

5'-most EST xpa700794387.h1
 Method BLASTX
 NCBI GI g2529685
 BLAST score 644
 E value 2.0e-67
 Match length 150
 % identity 80
 NCBI Description (AC002535) putative dimethyladenosine transferase
 [Arabidopsis thaliana]

Seq. No. 26213
 Contig ID 136668_1.R1040
 5'-most EST jC-gmfl02220063f03d1
 Method BLASTX
 NCBI GI g2880042
 BLAST score 273
 E value 6.0e-24
 Match length 79
 % identity 61
 NCBI Description (AC002340) putative 3-hydroxyisobutyryl-coenzyme A
 hydrolase [Arabidopsis thaliana]

Seq. No. 26214
 Contig ID 136670_2.R1040
 5'-most EST rca700997758.h1

Seq. No. 26215
 Contig ID 136688_1.R1040
 5'-most EST uC-gmropic087c03b1
 Method BLASTX
 NCBI GI g2129955
 BLAST score 199
 E value 1.0e-15
 Match length 55
 % identity 67
 NCBI Description photoassimilate-responsive protein PAR-1b precursor -
 common tobacco >gi_871487_emb_CAA58731_ (X83851) mRNA
 inducible by sucrose and salicylic acid expressed in
 sugar-accumulating tobacco plants [Nicotiana tabacum]

Seq. No. 26216
 Contig ID 136690_1.R1040
 5'-most EST ncj700975715.h1

Seq. No. 26217
 Contig ID 136696_1.R1040
 5'-most EST ncj700975723.h1

Seq. No. 26218
 Contig ID 136710_1.R1040
 5'-most EST kmv700741711.h1

Seq. No. 26219
 Contig ID 136716_1.R1040
 5'-most EST ncj700975761.h1

Seq. No. 26220

Contig ID 136729_1.R1040
5'-most EST zsg701123246.h1

Seq. No. 26221
Contig ID 136742_1.R1040
5'-most EST ncj700975805.h1
Method BLASTX
NCBI GI g2864614
BLAST score 361
E value 2.0e-34
Match length 116
% identity 57
NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 26222
Contig ID 136748_1.R1040
5'-most EST g4302457
Method BLASTX
NCBI GI g3386609
BLAST score 271
E value 2.0e-23
Match length 172
% identity 47
NCBI Description (AC004665) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No. 26223
Contig ID 136758_1.R1040
5'-most EST uC-gmrominsoy071g11b1
Method BLASTX
NCBI GI g4567303
BLAST score 392
E value 9.0e-38
Match length 81
% identity 83
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]

Seq. No. 26224
Contig ID 136777_1.R1040
5'-most EST asn701141013.h1
Method BLASTX
NCBI GI g4580395
BLAST score 132
E value 3.0e-13
Match length 84
% identity 52
NCBI Description (AC007171) putative kinesin-related protein [Arabidopsis thaliana]

Seq. No. 26225
Contig ID 136790_1.R1040
5'-most EST ncj700975914.h1

Seq. No. 26226
Contig ID 136793_1.R1040
5'-most EST ncj700978696.h1

Contig ID 136879_1.R1040
5'-most EST bth700846149.h1

Seq. No. 26235
Contig ID 136884_1.R1040
5'-most EST zzp700830287.h1
Method BLASTX
NCBI GI g3063471
BLAST score 357
E value 6.0e-34
Match length 123
% identity 56
NCBI Description (AC003981) F22013.33 [Arabidopsis thaliana]

Seq. No. 26236
Contig ID 136903_1.R1040
5'-most EST ncj700976415.h1

Seq. No. 26237
Contig ID 136947_1.R1040
5'-most EST jex700907988.h1
Method BLASTN
NCBI GI g3894098
BLAST score 285
E value 1.0e-159
Match length 809
% identity 86
NCBI Description Pisum sativum mRNA for protein encoded by MCM3 gene,
partial

Seq. No. 26238
Contig ID 137008_1.R1040
5'-most EST ncj700976718.h1
Method BLASTX
NCBI GI g2252840
BLAST score 155
E value 1.0e-10
Match length 64
% identity 45
NCBI Description (AF013293) contains regions of similarity to Haemophilus
influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No. 26239
Contig ID 137009_1.R1040
5'-most EST dpv701097153.h1
Method BLASTX
NCBI GI g3249066
BLAST score 387
E value 2.0e-37
Match length 130
% identity 64
NCBI Description (AC004473) Similar to S. cerevisiae SIK1P protein
gb_984964. ESTs gb_F15433 and gb_AA395158 come from this
gene. [Arabidopsis thaliana]

Seq. No. 26240
Contig ID 137019_1.R1040

5'-most EST ncj700976735.h1

Seq. No. 26241
 Contig ID 137024_1.R1040
 5'-most EST ncj700980607.h1
 Method BLASTX
 NCBI GI g464365
 BLAST score 194
 E value 4.0e-15
 Match length 54
 % identity 63
 NCBI Description PEROXIDASE P7 >gi_66306_pir__OPNB7 peroxidase (EC 1.11.1.7)
 - turnip

Seq. No. 26242
 Contig ID 137027_1.R1040
 5'-most EST ncj700976748.h1
 Method BLASTX
 NCBI GI g4220445
 BLAST score 166
 E value 1.0e-11
 Match length 124
 % identity 6
 NCBI Description (AC006216) Similar to gi_3004555 F19F24.14 salt inducible protein homolog from Arabidopsis thaliana BAC gb_AC003673. [Arabidopsis thaliana]

Seq. No. 26243
 Contig ID 137035_1.R1040
 5'-most EST fua701037758.h1
 Method BLASTX
 NCBI GI g3242721
 BLAST score 288
 E value 7.0e-26
 Match length 84
 % identity 68
 NCBI Description (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis thaliana]

Seq. No. 26244
 Contig ID 137082_1.R1040
 5'-most EST ncj700980969.h1
 Method BLASTX
 NCBI GI g3402684
 BLAST score 237
 E value 6.0e-20
 Match length 127
 % identity 39
 NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26245
 Contig ID 137088_1.R1040
 5'-most EST ncj700976860.h1
 Method BLASTN
 NCBI GI g1370143
 BLAST score 77
 E value 2.0e-35

000001-9104350

Match length 179
% identity 91
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB11B

Seq. No. 26246
Contig ID 137098_1.R1040
5'-most EST uC-gmrpic033g02b1
Method BLASTX
NCBI GI g1669655
BLAST score 263
E value 1.0e-22
Match length 113
% identity 50
NCBI Description (X95962) CER3 [Arabidopsis thaliana]

Seq. No. 26247
Contig ID 137108_1.R1040
5'-most EST vzy700752796.h1

Seq. No. 26248
Contig ID 137125_1.R1040
5'-most EST ncj700976924.h1

Seq. No. 26249
Contig ID 137148_1.R1040
5'-most EST ncj700976970.h1
Method BLASTX
NCBI GI g4454033
BLAST score 284
E value 1.0e-25
Match length 97
% identity 48
NCBI Description (AL035394) putative potassium transport protein [Arabidopsis thaliana]

Seq. No. 26250
Contig ID 137173_1.R1040
5'-most EST txt700735556.h1
Method BLASTX
NCBI GI g3157949
BLAST score 302
E value 3.0e-27
Match length 94
% identity 66
NCBI Description (AC002131) Similar to glucan endo-1,3-beta-D-glucosidase precursor gb_Z28697 from Nicotiana tabacum: ESTs gb_Z18185 and gb_AA605362 come from this gene. [Arabidopsis thaliana]

Seq. No. 26251
Contig ID 137186_1.R1040
5'-most EST ncj700977123.h1

Seq. No. 26252
Contig ID 137188_1.R1040
5'-most EST fC-gmfl700903880a1
Method BLASTX
NCBI GI g3688600

BLAST score 2672
E value 0.0e+00
Match length 610
% identity 76
NCBI Description (AB009030) beta-Amyrin Synthase [Panax ginseng]

Seq. No. 26253
Contig ID 137192_1.R1040
5'-most EST jC-gmst02400069g05a1
Method BLASTX
NCBI GI g2499005
BLAST score 202
E value 1.0e-15
Match length 109
% identity 42
NCBI Description 4-METHYL-5(B-HYDROXYETHYL)-THIAZOLE MONOPHOSPHATE BIOSYNTHESIS ENZYME >gi_1100872 (U34923) ThiJ [Escherichia coli] >gi_1773108 (U82664) 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein [Escherichia coli] >gi_1786626 (AE000148) 4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate synthesis [Escherichia coli]

Seq. No. 26254
Contig ID 137221_1.R1040
5'-most EST ncj700977219.h1

Seq. No. 26255
Contig ID 137222_1.R1040
5'-most EST ncj700977222.h1

Seq. No. 26256
Contig ID 137246_1.R1040
5'-most EST uC-gmrominsoy220d06b1
Method BLASTX
NCBI GI g3096947
BLAST score 186
E value 8.0e-30
Match length 117
% identity 54
NCBI Description (Y16327) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]

Seq. No. 26257
Contig ID 137248_1.R1040
5'-most EST fde700874237.h1
Method BLASTX
NCBI GI g4309731
BLAST score 313
E value 5.0e-29
Match length 97
% identity 62
NCBI Description (AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26258
Contig ID 137259_1.R1040
5'-most EST uC-gmrominsoy194b12b1

Method BLASTX
 NCBI GI g4432863
 BLAST score 606
 E value 2.0e-73
 Match length 200
 % identity 73
 NCBI Description (AC006300) putative phosphate/phosphoenolpyruvate translocator protein [Arabidopsis thaliana]

Seq. No. 26259
 Contig ID 137268_1.R1040
 5'-most EST ncj700977293.h1

Seq. No. 26260
 Contig ID 137291_1.R1040
 5'-most EST jC-gmf102220073g03a1
 Method BLASTX
 NCBI GI g2245039
 BLAST score 185
 E value 1.0e-13
 Match length 97
 % identity 49
 NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26261
 Contig ID 137291_2.R1040
 5'-most EST kl1701208291.h1
 Method BLASTX
 NCBI GI g2245039
 BLAST score 160
 E value 9.0e-11
 Match length 73
 % identity 51
 NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26262
 Contig ID 137291_3.R1040
 5'-most EST fde700873901.h1

Seq. No. 26263
 Contig ID 137314_1.R1040
 5'-most EST ncj700977374.h1

Seq. No. 26264
 Contig ID 137325_1.R1040
 5'-most EST ncj700983016.h1

Seq. No. 26265
 Contig ID 137365_1.R1040
 5'-most EST asn701138469.h1

Seq. No. 26266
 Contig ID 137378_1.R1040
 5'-most EST kl1701211957.h1
 Method BLASTX
 NCBI GI g3582436
 BLAST score 487

E value 5.0e-49
 Match length 145
 % identity 61
 NCBI Description (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]

Seq. No. 26267
 Contig ID 137378_2.R1040
 5'-most EST jC-gmle01810012d02a1
 Method BLASTX
 NCBI GI g3582436
 BLAST score 295
 E value 8.0e-45
 Match length 145
 % identity 61
 NCBI Description (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]

Seq. No. 26268
 Contig ID 137401_1.R1040
 5'-most EST uC-gmflminsoy030c07b1
 Method BLASTX
 NCBI GI g3482920
 BLAST score 188
 E value 4.0e-14
 Match length 112
 % identity 43
 NCBI Description (AC003970) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 26269
 Contig ID 137408_1.R1040
 5'-most EST ncj700977523.h1

Seq. No. 26270
 Contig ID 137415_1.R1040
 5'-most EST zzp700832246.h1
 Method BLASTX
 NCBI GI g3168840
 BLAST score 147
 E value 3.0e-09
 Match length 63
 % identity 41
 NCBI Description (U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No. 26271
 Contig ID 137418_1.R1040
 5'-most EST fua701038626.h1
 Method BLASTX
 NCBI GI g4455300
 BLAST score 307
 E value 6.0e-53
 Match length 156
 % identity 64
 NCBI Description (AL035528) putative pectate lyase A11 (fragment) [Arabidopsis thaliana]

Seq. No. 26272
 Contig ID 137418_2.R1040
 5'-most EST jex700905217.h1

Seq. No. 26273
Contig ID 137453_1.R1040
5'-most EST ncj700977616.h1

Seq. No. 26274
Contig ID 137457_1.R1040
5'-most EST leu701146856.h1
Method BLASTX
NCBI GI g537317
BLAST score 1219
E value 1.0e-134
Match length 335
% identity 74
NCBI Description (L36157) peroxidase [Medicago sativa]

Seq. No. 26275
Contig ID 137484_1.R1040
5'-most EST ncj700977666.h1

Seq. No. 26276
Contig ID 137486_1.R1040
5'-most EST ncj700977668.h1
Method BLASTX
NCBI GI g4240207
BLAST score 231
E value 5.0e-19
Match length 141
% identity 43
NCBI Description (AB020666) KIAA0859 protein [Homo sapiens]

Seq. No. 26277
Contig ID 137517_1.R1040
5'-most EST jC-gmfl02220078h08a1

Seq. No. 26278
Contig ID 137534_1.R1040
5'-most EST ncj700977745.h1
Method BLASTX
NCBI GI g2827528
BLAST score 200
E value 8.0e-16
Match length 67
% identity 54
NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 26279
Contig ID 137549_1.R1040
5'-most EST jC-gmfl02220079b03d1

Seq. No. 26280
Contig ID 137574_1.R1040
5'-most EST ncj700977809.h1

Seq. No. 26281
Contig ID 137576_1.R1040
5'-most EST zzp700830316.h1

Seq. No. 26282
 Contig ID 137581_1.R1040
 5'-most EST ncj700977821.h1
 Method BLASTX
 NCBI GI g1184077
 BLAST score 215
 E value 2.0e-17
 Match length 109
 % identity 2
 NCBI Description (U42445) Cf-2.2 [*Lycopersicon pimpinellifolium*]

Seq. No. 26283
 Contig ID 137593_1.R1040
 5'-most EST ncj700977844.h1

Seq. No. 26284
 Contig ID 137610_1.R1040
 5'-most EST vzy700755310.h1
 Method BLASTX
 NCBI GI g4567095
 BLAST score 290
 E value 4.0e-26
 Match length 80
 % identity 64
 NCBI Description (AF129516) fertilization-independent endosperm protein
 [*Arabidopsis thaliana*]

Seq. No. 26285
 Contig ID 137621_1.R1040
 5'-most EST smc700746759.h1

Seq. No. 26286
 Contig ID 137632_1.R1040
 5'-most EST kmv700738119.h1
 Method BLASTX
 NCBI GI g3451463
 BLAST score 246
 E value 9.0e-21
 Match length 128
 % identity 41
 NCBI Description (AL031349) hypothetical protein [*Schizosaccharomyces pombe*]

Seq. No. 26287
 Contig ID 137634_1.R1040
 5'-most EST uC-gmflminsoy078b08b1

Seq. No. 26288
 Contig ID 137639_1.R1040
 5'-most EST ncj700977918.h1

Seq. No. 26289
 Contig ID 137647_1.R1040
 5'-most EST ncj700977927.h1

Seq. No. 26290
 Contig ID 137667_1.R1040

5'-most EST ncj700977960.h1

Seq. No. 26291
 Contig ID 137676_1.R1040
 5'-most EST gsv701051166.h1
 Method BLASTX
 NCBI GI g2499931
 BLAST score 724
 E value 1.0e-76
 Match length 183
 % identity 77
 NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT)
 >gi_2129534_pir_S71272 adenine phosphoribosyltransferase
 (EC 2.4.2.7) - Arabidopsis thaliana
 >gi_1321681_emb_CAA65609_ (X96866) adenine
 phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No. 26292
 Contig ID 137677_1.R1040
 5'-most EST ncj700986622.h1

Seq. No. 26293
 Contig ID 137695_1.R1040
 5'-most EST jex700905884.h1

Seq. No. 26294
 Contig ID 137703_1.R1040
 5'-most EST ncj700978013.h1
 Method BLASTN
 NCBI GI g2695860
 BLAST score 67
 E value 2.0e-29
 Match length 146
 % identity 90
 NCBI Description Pisum sativum mRNA for
 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase, clone
 pPS40

Seq. No. 26295
 Contig ID 137707_1.R1040
 5'-most EST ncj700978019.h1

Seq. No. 26296
 Contig ID 137726_1.R1040
 5'-most EST pxt700942557.h1

Seq. No. 26297
 Contig ID 137729_1.R1040
 5'-most EST jsh701063755.h1

Seq. No. 26298
 Contig ID 137797_1.R1040
 5'-most EST pcp700992060.h1
 Method BLASTX
 NCBI GI g2062171
 BLAST score 166
 E value 8.0e-12

Match length 87
 % identity 45
 NCBI Description (AC001645) DNA binding protein (CDC27SH) isolog
 [Arabidopsis thaliana]

Seq. No. 26299
 Contig ID 137846_1.R1040
 5'-most EST vzy700750680.h1
 Method BLASTX
 NCBI GI g3287683
 BLAST score 243
 E value 9.0e-21
 Match length 110
 % identity 19
 NCBI Description (AC003979) Similar to apoptosis protein MA-3 gb_D50465 from
 Mus musculus. [Arabidopsis thaliana]

Seq. No. 26300
 Contig ID 137855_1.R1040
 5'-most EST rlr700895922.h1
 Method BLASTX
 NCBI GI g3080385
 BLAST score 179
 E value 7.0e-13
 Match length 92
 % identity 43
 NCBI Description (AL022603) serine/threonine protein kinase [Arabidopsis
 thaliana] >gi_3402760_emb_CAA20206.1_ (AL031187)
 serine/threonine kinase - like protein [Arabidopsis
 thaliana]

Seq. No. 26301
 Contig ID 137861_1.R1040
 5'-most EST asn701142772.h1

Seq. No. 26302
 Contig ID 137874_1.R1040
 5'-most EST leu701146878.h1

Seq. No. 26303
 Contig ID 137874_2.R1040
 5'-most EST leu701155970.h1

Seq. No. 26304
 Contig ID 137916_1.R1040
 5'-most EST ncj700978354.h1
 Method BLASTX
 NCBI GI g417570
 BLAST score 388
 E value 1.0e-58
 Match length 141
 % identity 87
 NCBI Description DIHYDROOROTATE DEHYDROGENASE PRECURSOR (DIHYDROOROTATE
 OXIDASE) (DHODEHASE) >gi_478676_pir_S23762 dihydroorotate
 oxidase (EC 1.3.3.1) - Arabidopsis thaliana
 >gi_16449_emb_CAA44695_ (X62909) dihydroorotate
 dehydrogenase [Arabidopsis thaliana]

Seq. No. 26305
 Contig ID 137917 1.R1040
 5'-most EST zhf700955804.h1

Seq. No. 26306
 Contig ID 137924 1.R1040
 5'-most EST zhf700964637.h1
 Method BLASTX
 NCBI GI g1084334
 BLAST score 348
 E value 7.0e-33
 Match length 81
 % identity 80
 NCBI Description calcium-dependent protein kinase (EC 2.7.1.-) 1 -
 Arabidopsis thaliana >gi_604880_dbj_BAA04829_ (D21805)
 calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No. 26307
 Contig ID 137933 1.R1040
 5'-most EST ncj700978380.h1

Seq. No. 26308
 Contig ID 137950 1.R1040
 5'-most EST ncj700978404.h1
 Method BLASTX
 NCBI GI g2462825
 BLAST score 234
 E value 1.0e-26
 Match length 73
 % identity 85
 NCBI Description (AF000657) contains Procite 'RNP1' putative RNA-binding
 region [Arabidopsis thaliana]

Seq. No. 26309
 Contig ID 137955 1.R1040
 5'-most EST fde700874521.h1
 Method BLASTX
 NCBI GI g4204793
 BLAST score 588
 E value 6.0e-84
 Match length 273
 % identity 31
 NCBI Description (U52079) P-glycoprotein [Solanum tuberosum]

Seq. No. 26310
 Contig ID 137960 1.R1040
 5'-most EST uC-gmrominsoy205f03b1
 Method BLASTN
 NCBI GI g3821780
 BLAST score 34
 E value 2.0e-09
 Match length 34
 % identity 59
 NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 26311

[illegible]

[illegible]

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Seq. No.          26333
Contig ID         138269_1.R1040
5'-most EST      uC-gmflminsoy042e10b1
Method            BLASTX
NCBI_GI           g2462831
BLAST score       200
E value           2.0e-15
Match length      78
% identity        62
NCBI Description  (AF000657) hypothetical
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Seq. No.	26335
Contig ID	138291_1.R1040
5'-most EST	ncj700978978.h1

Seq. No.	26337
Contig ID	138314_1.R1040
5'-most EST	rca701000761.h1

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Seq. No.          26338
Contig ID         138324_1.R1040
5'-most EST      jC-gmst02400053a11d1
Method           BLASTX
NCBI GI          g2145356
BLAST score      246
E value          6.0e-21
Match length     56
% identity       77
NCBI Description (Y11122) HD-Zip protein [Arabidopsis thaliana] >gi_3132474
                  (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]

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Seq. No.	26339
Contig ID	138333_1.R1040
5'-most EST	ncj700979044.h1

```
Seq. No.          26340
Contig ID         138341_1.R1040
5'-most EST      jC-gmst02400063h12a1
Method            BLASTN
NCBI GI           g2352083
BLAST score       134
E value           4.0e-69
Match length      410
```


% identity 85
 NCBI Description Arabidopsis thaliana serine/threonine kinase (SIK1) mRNA, complete cds

Seq. No. 26341
 Contig ID 138373_1.R1040
 5'-most EST gsv701044663.h1

Seq. No. 26342
 Contig ID 138400_1.R1040
 5'-most EST kll701208735.h1
 Method BLASTX
 NCBI GI g4580397
 BLAST score 177
 E value 4.0e-13
 Match length 98
 % identity 42
 NCBI Description (AC007171) putative RNA helicase [Arabidopsis thaliana]

Seq. No. 26343
 Contig ID 138456_1.R1040
 5'-most EST ncj700979345.h1
 Method BLASTX
 NCBI GI g4544460
 BLAST score 280
 E value 1.0e-24
 Match length 146
 % identity 39
 NCBI Description (AC006592) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No. 26344
 Contig ID 138462_1.R1040
 5'-most EST wrq700787528.h1
 Method BLASTX
 NCBI GI g1076274
 BLAST score 357
 E value 9.0e-34
 Match length 143
 % identity 49
 NCBI Description cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)

Seq. No. 26345
 Contig ID 138471_1.R1040
 5'-most EST ncj700987631.h1
 Method BLASTX
 NCBI GI g4454043
 BLAST score 167
 E value 6.0e-12
 Match length 54
 % identity 56
 NCBI Description (AL035394) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 26346
 Contig ID 138475_1.R1040
 5'-most EST jC-gmro02910034f08a1

Contig ID	138616_1.R1040
5'-most EST	ncj700979642.h2
Seq. No.	26363
Contig ID	138629_1.R1040
5'-most EST	jC-gmf102220115d06a1
Seq. No.	26364
Contig ID	138652_1.R1040
5'-most EST	dpv701100659.h1
Seq. No.	26365
Contig ID	138675_1.R1040
5'-most EST	hrw701056979.h1
Seq. No.	26366
Contig ID	138675_2.R1040
5'-most EST	wrg700786026.h2
Seq. No.	26367
Contig ID	138692_1.R1040
5'-most EST	ncj700979777.h2
Seq. No.	26368
Contig ID	138721_1.R1040
5'-most EST	jC-gmle01810064g11a1
Method	BLASTX
NCBI GI	g2529686
BLAST score	473
E value	2.0e-54
Match length	125
% identity	78
NCBI Description	(AC002535) putative G-beta-repeat containing protein, 5' partial [Arabidopsis thaliana]
Seq. No.	26369
Contig ID	138724_1.R1040
5'-most EST	ncj700979845.h2
Method	BLASTX
NCBI GI	g4539459
BLAST score	400
E value	4.0e-39
Match length	106
% identity	68
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]
Seq. No.	26370
Contig ID	138756_1.R1040
5'-most EST	pxt700943842.h1
Method	BLASTX
NCBI GI	g1170409
BLAST score	369
E value	1.0e-35
Match length	93
% identity	76
NCBI Description	HOMEBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22) >gi_549887 (U09336) homeobox protein [Arabidopsis thaliana]

>gi_549888 (U09337) homeobox protein [Arabidopsis thaliana]
 >gi_4490724_emb_CAB38927.1_ (AL035709) homeobox protein
 HAT22 [Arabidopsis thaliana]

Seq. No. 26371
 Contig ID 138767_1.R1040
 5'-most EST g4396113
 Method BLASTX
 NCBI GI g3402704
 BLAST score 547
 E value 7.0e-56
 Match length 187
 % identity 63
 NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26372
 Contig ID 138794_1.R1040
 5'-most EST ncj700980025.h1
 Method BLASTN
 NCBI GI g2264314
 BLAST score 33
 E value 7.0e-09
 Match length 105
 % identity 83
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 MQK4, complete sequence [Arabidopsis thaliana]

Seq. No. 26373
 Contig ID 138812_1.R1040
 5'-most EST ncj700980082.h1
 Method BLASTX
 NCBI GI g3123130
 BLAST score 208
 E value 4.0e-29
 Match length 108
 % identity 45
 NCBI Description HYPOTHETICAL 61.8 KD TRP-ASP REPEATS CONTAINING PROTEIN
 T32G6.2 IN CHROMOSOME II >gi_2618685 (AC002510) putative
 small nuclear ribonucleoprotein Prp4p [Arabidopsis
 thaliana] >gi_3241948 (AC004625) putative small nuclear
 ribonucleoprotein Prp4p [Arabidopsis thaliana]

Seq. No. 26374
 Contig ID 138816_1.R1040
 5'-most EST epx701104215.h1

Seq. No. 26375
 Contig ID 138821_1.R1040
 5'-most EST ncj700980106.h1
 Method BLASTX
 NCBI GI g2501491
 BLAST score 169
 E value 2.0e-12
 Match length 81
 % identity 43
 NCBI Description FLAVONOL 3-O-GLUCOSYLTRANSFERASE 1 (UDP-GLUCOSE FLAVONOID
 3-O-GLUCOSYLTRANSFERASE 1) >gi_542014_pir__S41950

056649-100000

Seq. No.	26398
Contig ID	139195_1.R1040
5'-most EST	epx701104057.h1

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Seq. No.          26399
Contig ID         139204 2.R1040
5'-most EST      ncj700986459.h1
Method            BLASTX
NCBI GI           g3201554
BLAST score       202
E value           5.0e-18
Match length      103
% identity        50
NCBI Description  (AJ006501) beta-D-glucosidase [Tropaeolum majus]

```

```
Seq. No.          26400
Contig ID         139207_1.R1040
5'-most EST      g4301925
Method            BLASTX
NCBI GI           g3063466
BLAST score       132
E value           2.0e-16
Match length      82
% identity        56
NCBI Description  (AC003981) F22013.28 [Arabidopsis thaliana]
```

```
Seq. No.          26401
Contig ID         139217_1.R1040
5'-most EST      uC-gmropic065c09b1
Method            BLASTX
NCBI GI           g1176658
BLAST score       271
E value           1.0e-23
Match length      111
% identity        50
NCBI Description  HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II
                  >gi_726363 (U23168) No definition line found
                  [Caenorhabditis elegans]
```

```
Seq. No.      26402
Contig ID     139232_2.R1040
5'-most EST   zhf700952549.h1
```

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Seq. No.          26403
Contig ID         139267_1.R1040
5'-most EST      pxt700945232.h1
Method            BLASTX
NCBI GI           g3096919
BLAST score       576
E value           2.0e-59
Match length      142
```


% identity	77
NCBI Description	(AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	26404
Contig ID	139279_1.R1040
5'-most EST	ncj700980985.h1
Seq. No.	26405
Contig ID	139286_1.R1040
5'-most EST	ncj700980994.h1
Method	BLASTX
NCBI GI	g3355478
BLAST score	163
E value	3.0e-11
Match length	97
% identity	41
NCBI Description	(AC004218) hypothetical protein [Arabidopsis thaliana]
Seq. No.	26406
Contig ID	139289_1.R1040
5'-most EST	leu701152205.h1
Method	BLASTX
NCBI GI	g3603401
BLAST score	351
E value	4.0e-33
Match length	111
% identity	59
NCBI Description	(AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]
Seq. No.	26407
Contig ID	139291_1.R1040
5'-most EST	uC-gmflminsoy042c11b1
Method	BLASTX
NCBI GI	g2651302
BLAST score	486
E value	5.0e-49
Match length	141
% identity	63
NCBI Description	(AC002336) hypothetical protein [Arabidopsis thaliana]
Seq. No.	26408
Contig ID	139303_1.R1040
5'-most EST	ncj700981028.h1
Seq. No.	26409
Contig ID	139323_1.R1040
5'-most EST	ncj700981065.h1
Method	BLASTX
NCBI GI	g4006854
BLAST score	238
E value	3.0e-20
Match length	96
% identity	53
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]
Seq. No.	26410

Contig ID 139338 1.R1040
5'-most EST leu701152581.h1

Seq. No. 26411
Contig ID 139339 1.R1040
5'-most EST gsv701055401.h1
Method BLASTX
NCBI GI g3785989
BLAST score 539
E value 3.0e-55
Match length 139
% identity 75
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]

Seq. No. 26412
Contig ID 139345 1.R1040
5'-most EST wrq700788384.h1
Method BLASTX
NCBI GI g629562
BLAST score 812
E value 4.0e-87
Match length 172
% identity 87
NCBI Description sulfate adenylyltransferase (EC 2.7.7.4) - Arabidopsis thaliana >gi_2129743_pir_S68024 sulfate adenylyltransferase (EC 2.7.7.4) precursor (clone APS2) - Arabidopsis thaliana >gi_487404_emb_CAA55799_ (X79210) sulfate adenylyltransferase [Arabidopsis thaliana] >gi_1228104 (U06276) ATP sulfurylase [Arabidopsis thaliana] >gi_1378028 (U40715) ATP sulfurylase precursor [Arabidopsis thaliana] >gi_1575324 (U59737) ATP sulfurylase [Arabidopsis thaliana]

Seq. No. 26413
Contig ID 139346 1.R1040
5'-most EST uC-gmr0noir008f03b1
Method BLASTX
NCBI GI g2828289
BLAST score 154
E value 5.0e-10
Match length 59
% identity 51
NCBI Description (AL021687) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26414
Contig ID 139346 2.R1040
5'-most EST zzp700833537.h1

Seq. No. 26415
Contig ID 139400 1.R1040
5'-most EST g5126598

Seq. No. 26416
Contig ID 139404 1.R1040
5'-most EST ncj700981213.h1
Method BLASTX
NCBI GI g116923

BLAST score 172
E value 5.0e-12
Match length 62
% identity 55
NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26425
Contig ID 139546_1.R1040
5'-most EST ncj700981436.h1
Method BLASTX
NCBI GI g3201554
BLAST score 558
E value 1.0e-83
Match length 228
% identity 66
NCBI Description (AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No. 26426
Contig ID 139549_1.R1040
5'-most EST vzy700752472.h1

Seq. No. 26427
Contig ID 139560_1.R1040
5'-most EST zhf700958364.h1
Method BLASTN
NCBI GI g2104674
BLAST score 89
E value 2.0e-42
Match length 219
% identity 91
NCBI Description V.faba mRNA for transcription factor containing bZIP

Seq. No. 26428
Contig ID 139572_1.R1040
5'-most EST ncj700981485.h1

Seq. No. 26429
Contig ID 139578_1.R1040
5'-most EST ncj700981491.h1

Seq. No. 26430
Contig ID 139592_1.R1040
5'-most EST uC-gmropic012b06b1

Seq. No. 26431
Contig ID 139596_1.R1040
5'-most EST jC-gmle01810010b04a1

Seq. No. 26432
Contig ID 139609_1.R1040
5'-most EST ncj700981547.h1

Seq. No. 26433
Contig ID 139610_1.R1040
5'-most EST jC-gmle01810015a04d1

Seq. No. 26434

% identity	50
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]
Seq. No.	26442
Contig ID	139701_1.R1040
5'-most EST	leu701150580.h1
Seq. No.	26443
Contig ID	139717_1.R1040
5'-most EST	ncj700981712.h1
Seq. No.	26444
Contig ID	139790_1.R1040
5'-most EST	ncj700981842.h1
Method	BLASTX
NCBI GI	g2980806
BLAST score	145
E value	3.0e-09
Match length	36
% identity	69
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]
Seq. No.	26445
Contig ID	139808_1.R1040
5'-most EST	zpv700759887.h1
Seq. No.	26446
Contig ID	139809_1.R1040
5'-most EST	hrw701060688.h1
Method	BLASTX
NCBI GI	g282964
BLAST score	344
E value	2.0e-32
Match length	81
% identity	75
NCBI Description	transforming protein (myb) homolog (clone myb.Ph3) - garden petunia >gi_20563_emb_CAA78386_ (Z13996) protein 1 [Petunia x hybrida]
Seq. No.	26447
Contig ID	139827_1.R1040
5'-most EST	jC-gmfl02220114e07d1
Seq. No.	26448
Contig ID	139828_1.R1040
5'-most EST	xpa700792448.h1
Method	BLASTX
NCBI GI	g4454026
BLAST score	384
E value	1.0e-41
Match length	138
% identity	65
NCBI Description	(AL035394) phosphatase like protein [Arabidopsis thaliana]
Seq. No.	26449
Contig ID	139836_1.R1040
5'-most EST	ncj700981939.h1

Method	BLASTN
NCBI GI	g559505
BLAST score	128
E value	1.0e-65
Match length	368
% identity	84
NCBI Description	P.hybrida mRNA for S-adenosylmethionine-synthetase
Seq. No.	26450
Contig ID	139845_1.R1040
5'-most EST	ncj700981952.h1
Method	BLASTX
NCBI GI	g3335353
BLAST score	194
E value	4.0e-15
Match length	78
% identity	47
NCBI Description	(AC004512) Similar to cytochrome P450 gb_X90458 from A. thaliana. [Arabidopsis thaliana]
Seq. No.	26451
Contig ID	139861_1.R1040
5'-most EST	kl1701205476.h1
Method	BLASTX
NCBI GI	g3646336
BLAST score	392
E value	8.0e-38
Match length	121
% identity	68
NCBI Description	(AJ001682) MdMADS9 [Malus domestica]
Seq. No.	26452
Contig ID	139874_1.R1040
5'-most EST	dpv701100857.h1
Method	BLASTX
NCBI GI	g1429226
BLAST score	315
E value	6.0e-29
Match length	96
% identity	64
NCBI Description	(X98861) TFIIA [Arabidopsis thaliana]
Seq. No.	26453
Contig ID	139889_1.R1040
5'-most EST	uC-gmrominsoy108e12b1
Method	BLASTX
NCBI GI	g2497034
BLAST score	177
E value	8.0e-13
Match length	109
% identity	41
NCBI Description	HYPOTHETICAL 55.5 KD PROTEIN ZK1128.2 IN CHROMOSOME IIII >gi_3881502_emb_CAA87421_ (Z47357) ZK1128.2 [Caenorhabditis elegans]
Seq. No.	26454
Contig ID	139937_1.R1040

5'-most EST fua701040927.h1

Seq. No. 26455
 Contig ID 139941_1.R1040
 5'-most EST gsf700698307.h1

Seq. No. 26456
 Contig ID 139965_1.R1040
 5'-most EST ncj700983310.h1
 Method BLASTN
 NCBI GI g1217993
 BLAST score 217
 E value 1.0e-119
 Match length 413
 % identity 88
 NCBI Description Glycine max dynamin-like protein SDL12A mRNA, complete cds

Seq. No. 26457
 Contig ID 139977_1.R1040
 5'-most EST gsv701046585.h1

Seq. No. 26458
 Contig ID 139989_1.R1040
 5'-most EST asn701141023.h1
 Method BLASTX
 NCBI GI g2880047
 BLAST score 540
 E value 3.0e-57
 Match length 181
 % identity 69
 NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26459
 Contig ID 140018_1.R1040
 5'-most EST kl1701205510.h1
 Method BLASTX
 NCBI GI g3249098
 BLAST score 245
 E value 2.0e-20
 Match length 99
 % identity 52
 NCBI Description (AC003114) ESTs gb_T04610, gb_N38459, gb_T45174, gb_R30481 and gb_N64971 come from this gene. [Arabidopsis thaliana]

Seq. No. 26460
 Contig ID 140025_1.R1040
 5'-most EST g5676821

Seq. No. 26461
 Contig ID 140029_1.R1040
 5'-most EST gsv701053383.h1

Seq. No. 26462
 Contig ID 140030_1.R1040
 5'-most EST eep700863841.h1

Seq. No. 26463

Seq. No. 26482
 Contig ID 140304_1.R1040
 5'-most EST kmv700739574.h1
 Method BLASTX
 NCBI GI g2262157
 BLAST score 361
 E value 1.0e-34
 Match length 96
 % identity 69
 NCBI Description (AC002329) putative ligand-gated ion channel protein
 [Arabidopsis thaliana]

Seq. No. 26483
 Contig ID 140329_1.R1040
 5'-most EST ncj700982775.h1
 Method BLASTX
 NCBI GI g3785977
 BLAST score 233
 E value 1.0e-19
 Match length 92
 % identity 53
 NCBI Description (AC005560) putative growth regulator protein [Arabidopsis
 thaliana]

Seq. No. 26484
 Contig ID 140330_1.R1040
 5'-most EST leu701156303.h1
 Method BLASTX
 NCBI GI g629561
 BLAST score 440
 E value 2.0e-43
 Match length 217
 % identity 41
 NCBI Description SRG1 protein - Arabidopsis thaliana
 >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis
 thaliana]

Seq. No. 26485
 Contig ID 140382_1.R1040
 5'-most EST ncj700982879.h1
 Method BLASTX
 NCBI GI g3152572
 BLAST score 322
 E value 3.0e-30
 Match length 78
 % identity 90
 NCBI Description (AC002986) Contains homology to DNAJ heatshock protein
 gb_U32803 from Haemophilus influenzae. [Arabidopsis
 thaliana]

Seq. No. 26486
 Contig ID 140385_1.R1040
 5'-most EST jsh701064350.h1
 Method BLASTX
 NCBI GI g4006918
 BLAST score 319
 E value 2.0e-29

Match length	121
% identity	53
NCBI Description	(Z99708) peroxidase like protein [Arabidopsis thaliana]
Seq. No.	26487
Contig ID	140394_1.R1040
5'-most EST	kl1701212683.h1
Seq. No.	26488
Contig ID	140395_1.R1040
5'-most EST	ncj700982901.h1
Seq. No.	26489
Contig ID	140399_1.R1040
5'-most EST	jex700907547.h1
Seq. No.	26490
Contig ID	140416_1.R1040
5'-most EST	ncj700982958.h1
Method	BLASTX
NCBI GI	g2244833
BLAST score	263
E value	7.0e-23
Match length	137
% identity	44
NCBI Description	(Z97337) centromere protein homolog [Arabidopsis thaliana]
Seq. No.	26491
Contig ID	140421_1.R1040
5'-most EST	ncj700982975.h1
Seq. No.	26492
Contig ID	140470_1.R1040
5'-most EST	kwa701015680.h1
Seq. No.	26493
Contig ID	140493_1.R1040
5'-most EST	ncj700983103.h1
Method	BLASTN
NCBI GI	g2104523
BLAST score	35
E value	3.0e-10
Match length	67
% identity	88
NCBI Description	Arabidopsis thaliana BAC T10M13 from chromosome IV, from 10.8 cM to 11.6 cM, complete sequence
Seq. No.	26494
Contig ID	140533_1.R1040
5'-most EST	gsv701046889.h1
Seq. No.	26495
Contig ID	140543_1.R1040
5'-most EST	g5752614
Seq. No.	26496
Contig ID	140551_1.R1040

031619

BLAST score 425
 E value 4.0e-42
 Match length 112
 % identity 73
 NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No. 26506
 Contig ID 140695_1.R1040
 5'-most EST pmv700891626.h1
 Method BLASTX
 NCBI GI g2244987
 BLAST score 346
 E value 1.0e-32
 Match length 156
 % identity 45
 NCBI Description (Z97340) similarity to protein kinase - slime mold (Dictyostelium) [Arabidopsis thaliana]

Seq. No. 26507
 Contig ID 140696_1.R1040
 5'-most EST jC-gmro02910012b11a1

Seq. No. 26508
 Contig ID 140697_1.R1040
 5'-most EST jC-gmro02910019b04d1

Seq. No. 26509
 Contig ID 140706_1.R1040
 5'-most EST ncj700983470.h1

Seq. No. 26510
 Contig ID 140729_1.R1040
 5'-most EST zzp700831407.h1
 Method BLASTX
 NCBI GI g2154997
 BLAST score 421
 E value 4.0e-41
 Match length 196
 % identity 46
 NCBI Description (Y12503) Man9-mannosidase [Sus scrofa]

Seq. No. 26511
 Contig ID 140748_1.R1040
 5'-most EST cfl700863544.h1
 Method BLASTX
 NCBI GI g4490937
 BLAST score 245
 E value 8.0e-21
 Match length 126
 % identity 37
 NCBI Description (AJ132261) hypothetical helicase K12H4.8-like protein [Homo sapiens]

Seq. No. 26512
 Contig ID 140752_1.R1040
 5'-most EST jC-gmle01810060e10a1

Seq. No. 26520
 Contig ID 140837_1.R1040
 5'-most EST jC-gmst02400053a10d1

Seq. No. 26521
 Contig ID 140844_1.R1040
 5'-most EST zhf700964855.h1
 Method BLASTX
 NCBI GI g4218120
 BLAST score 277
 E value 1.0e-24
 Match length 61
 % identity 82
 NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No. 26522
 Contig ID 140880_1.R1040
 5'-most EST asn701136306.h1
 Method BLASTX
 NCBI GI g4455326
 BLAST score 675
 E value 4.0e-71
 Match length 171
 % identity 71
 NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 26523
 Contig ID 140888_1.R1040
 5'-most EST ncj700986805.h1

Seq. No. 26524
 Contig ID 140902_1.R1040
 5'-most EST pcp700995354.h1

Seq. No. 26525
 Contig ID 140916_1.R1040
 5'-most EST ncj700983850.h1

Seq. No. 26526
 Contig ID 140937_1.R1040
 5'-most EST ncj700983884.h1
 Method BLASTX
 NCBI GI g2352492
 BLAST score 559
 E value 3.0e-66
 Match length 197
 % identity 67
 NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No. 26527
 Contig ID 140957_1.R1040
 5'-most EST leu701152930.h1
 Method BLASTX
 NCBI GI g3785987

[illegible]

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Seq. No.          26550
Contig ID         141239_1.R1040
5'-most EST      ncj700984573.h1
Method            BLASTX
NCBI GI           g3212868
BLAST score       534
E value           2.0e-54
Match length      170
% identity        62
NCBI Description  (AC004005) unk
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Seq. No.          26552
Contig ID         141286_1.R1040
5'-most EST      ncj700984706.h1
Method            BLASTX
NCBI GI           g4490756
BLAST score       187
E value           2.0e-16
Match length      106
% identity        41
NCBI Description  (AL035708) hypothetical protein [Arabidopsis thaliana]
```

Seq. No.	26554
Contig ID	141303 1.R1040

5'-most EST jC-gmst02400055f01d1
 Method BLASTX
 NCBI GI g2288887
 BLAST score 164
 E value 3.0e-11
 Match length 44
 % identity 70
 NCBI Description (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3786002 (AC005499) mevalonate diphosphate decarboxylase [Arabidopsis thaliana]

Seq. No. 26555
 Contig ID 141332_1.R1040
 5'-most EST ncj700984770.h1
 Method BLASTX
 NCBI GI g3152559
 BLAST score 490
 E value 5.0e-49
 Match length 197
 % identity 49
 NCBI Description (AC002986) Similarity to A. thaliana gene product F21M12.20, gb_AC000132. EST gb_Z25651 comes from this gene. [Arabidopsis thaliana]

Seq. No. 26556
 Contig ID 141335_1.R1040
 5'-most EST epx701110420.h1

Seq. No. 26557
 Contig ID 141345_1.R1040
 5'-most EST ncj700984788.h1
 Method BLASTX
 NCBI GI g2244852
 BLAST score 207
 E value 1.0e-16
 Match length 51
 % identity 80
 NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26558
 Contig ID 141404_1.R1040
 5'-most EST ncj700984884.h1
 Method BLASTX
 NCBI GI g4204293
 BLAST score 183
 E value 6.0e-14
 Match length 83
 % identity 45
 NCBI Description (AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No. 26559
 Contig ID 141442_1.R1040
 5'-most EST leu701154394.h1

5'-most EST ncj700985611.h1
 Method BLASTX
 NCBI GI g2702268
 BLAST score 396
 E value 2.0e-38
 Match length 114
 % identity 66
 NCBI Description (AC003033) putative cellulase [Arabidopsis thaliana]

Seq. No. 26586
 Contig ID 141877_2.R1040
 5'-most EST epx701109545.h1
 Method BLASTX
 NCBI GI g2702268
 BLAST score 223
 E value 2.0e-18
 Match length 81
 % identity 57
 NCBI Description (AC003033) putative cellulase [Arabidopsis thaliana]

Seq. No. 26587
 Contig ID 141881_1.R1040
 5'-most EST ncj700985615.h1
 Method BLASTX
 NCBI GI g4210449
 BLAST score 362
 E value 5.0e-34
 Match length 273
 % identity 38
 NCBI Description (AB016471) ARR1 protein [Arabidopsis thaliana]

Seq. No. 26588
 Contig ID 141903_1.R1040
 5'-most EST pcp700995658.h1
 Method BLASTX
 NCBI GI g3805851
 BLAST score 400
 E value 6.0e-39
 Match length 102
 % identity 72
 NCBI Description (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 26589
 Contig ID 141943_1.R1040
 5'-most EST pmv700890950.h1

Seq. No. 26590
 Contig ID 141956_1.R1040
 5'-most EST ncj700985737.h1

Seq. No. 26591
 Contig ID 141997_1.R1040
 5'-most EST asn701132792.h1

Seq. No. 26592
 Contig ID 142003_1.R1040
 5'-most EST ncj700985810.h1

Seq. No.	26602
Contig ID	142117_1.R1040
5'-most EST	ncj700987991.h1
Method	BLASTN
NCBI GI	g4140025
BLAST score	186
E value	1.0e-100
Match length	428
% identity	86
NCBI Description	Vigna mungo UF3GaT mRNA for flavonoid 3-O-galactosyl transferase, complete cds
Seq. No.	26603
Contig ID	142123_1.R1040
5'-most EST	epx701105074.h1
Seq. No.	26604
Contig ID	142133_1.R1040
5'-most EST	smc700747118.h1
Seq. No.	26605
Contig ID	142139_1.R1040
5'-most EST	gsv701056689.h1
Seq. No.	26606
Contig ID	142148_1.R1040
5'-most EST	ncj700986016.h1
Seq. No.	26607
Contig ID	142193_1.R1040
5'-most EST	zhf700959032.h1
Seq. No.	26608
Contig ID	142193_2.R1040
5'-most EST	jex700906403.h1
Seq. No.	26609
Contig ID	142206_1.R1040
5'-most EST	uC-gmflminsoy075a05b1
Seq. No.	26610
Contig ID	142232_1.R1040
5'-most EST	jC-gmle01810022c01a1
Method	BLASTX
NCBI GI	g4490325
BLAST score	398
E value	7.0e-39
Match length	113
% identity	69
NCBI Description	(AL035656) hypothetical protein [Arabidopsis thaliana]
Seq. No.	26611
Contig ID	142237_1.R1040
5'-most EST	ncj700986140.h1
Method	BLASTX
NCBI GI	q2443887

NCBI Description (AF031194) S276 [Triticum aestivum]

Seq. No. 26621
Contig ID 142375_1.R1040
5'-most EST crh700854918.h1

Seq. No. 26622
Contig ID 142379_1.R1040
5'-most EST uC-gmflminsoy067b12b1

Seq. No. 26623
Contig ID 142385_1.R1040
5'-most EST ncj700986408.h1

Method BLASTX
NCBI GI g4185499
BLAST score 335
E value 4.0e-31
Match length 150
% identity 44

NCBI Description (AF096095) fertilization-independent seed 2 protein
[Arabidopsis thaliana] >gi_4185501 (AF096096)
fertilization-independent seed 2 protein [Arabidopsis
thaliana]

Seq. No. 26624
Contig ID 142400_1.R1040
5'-most EST zhf700964744.h1

Seq. No. 26625
Contig ID 142416_1.R1040
5'-most EST jC-gmro02800033e10a1

Method BLASTX
NCBI GI g2262173
BLAST score 441
E value 6.0e-44
Match length 112
% identity 78

NCBI Description (AC002329) NADPH thioredoxin reductase [Arabidopsis
thaliana]

Seq. No. 26626
Contig ID 142419_1.R1040
5'-most EST jex700906483.h1

Method BLASTX
NCBI GI g1345132
BLAST score 376
E value 8.0e-44
Match length 117
% identity 80

NCBI Description (U47029) ERECTA [Arabidopsis thaliana]
>gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase
[Arabidopsis thaliana] >gi_3075386 (AC004484) receptor
protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No. 26627
Contig ID 142424_1.R1040
5'-most EST kmv700740451.h1

Seq. No. 26654
 Contig ID 142716_1.R1040
 5'-most EST vzy700753607.h1

Seq. No. 26655
 Contig ID 142721_1.R1040
 5'-most EST kl1701212835.h1

Seq. No. 26656
 Contig ID 142733_2.R1040
 5'-most EST leu701151255.h1
 Method BLASTX
 NCBI GI g4103757
 BLAST score 256
 E value 3.0e-22
 Match length 55
 % identity 91
 NCBI Description (AF027376) MADS1 [Corylus avellana]

Seq. No. 26657
 Contig ID 142759_1.R1040
 5'-most EST pcp700990417.h1

Seq. No. 26658
 Contig ID 142792_1.R1040
 5'-most EST ncj700987043.h1
 Method BLASTX
 NCBI GI g3201554
 BLAST score 396
 E value 1.0e-66
 Match length 169
 % identity 76
 NCBI Description (AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No. 26659
 Contig ID 142801_1.R1040
 5'-most EST ncj700987054.h1

Seq. No. 26660
 Contig ID 142832_1.R1040
 5'-most EST uC-gmrominsoy111h09b1
 Method BLASTX
 NCBI GI g2459437
 BLAST score 197
 E value 3.0e-15
 Match length 77
 % identity 62
 NCBI Description (AC002332) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26661
 Contig ID 142837_1.R1040
 5'-most EST ncj700987110.h1

Seq. No. 26662
 Contig ID 142861_1.R1040
 5'-most EST uC-gmflminsoy007a10b1
 Method BLASTX

NCBI GI g4544436
 BLAST score 295
 E value 5.0e-28
 Match length 139
 % identity 49
 NCBI Description (AC006592) anthocyanidin-3-glucoside rhamnosyltransferase,
 3' partial [Arabidopsis thaliana]

Seq. No. 26663
 Contig ID 142866_1.R1040
 5'-most EST leu701156129.h1
 Method BLASTX
 NCBI GI g3242728
 BLAST score 221
 E value 9.0e-18
 Match length 204
 % identity 39
 NCBI Description (AC003040) unknown protein [Arabidopsis thaliana]

Seq. No. 26664
 Contig ID 142871_1.R1040
 5'-most EST ncj700987156.h1

Seq. No. 26665
 Contig ID 142883_1.R1040
 5'-most EST jC-gmst02400065e08a2
 Method BLASTX
 NCBI GI g2760839
 BLAST score 228
 E value 1.0e-18
 Match length 101
 % identity 49
 NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 26666
 Contig ID 142885_1.R1040
 5'-most EST dpv701100860.h1
 Method BLASTX
 NCBI GI g4193320
 BLAST score 465
 E value 7.0e-47
 Match length 99
 % identity 84
 NCBI Description (AF045473) histone deacetylase [Zea mays]

Seq. No. 26667
 Contig ID 142907_1.R1040
 5'-most EST jC-gmf102220137a09a1

Seq. No. 26668
 Contig ID 142913_1.R1040
 5'-most EST jC-gmf102220080b07a1

Seq. No. 26669
 Contig ID 142915_1.R1040
 5'-most EST ncj700987212.h1
 Method BLASTX

NCBI GI g3122595
 BLAST score 118
 E value 1.0e-10
 Match length 57
 % identity 55
 NCBI Description PROBABLE RNA-DEPENDENT HELICASE P72 (DEAD-BOX PROTEIN P72)
 >gi_1592565 (U59321) DEAD-box protein p72 [Homo sapiens]
 >gi_2832596_emb_CAB09792_ (Z97056) dJ434P1.3 [Homo sapiens]

Seq. No. 26670
 Contig ID 142920_1.R1040
 5'-most EST uC-gmropic037d11b1

Seq. No. 26671
 Contig ID 142923_1.R1040
 5'-most EST kmv700741889.h1

Seq. No. 26672
 Contig ID 142945_1.R1040
 5'-most EST eep700864944.h1

Seq. No. 26673
 Contig ID 142957_1.R1040
 5'-most EST uC-gmrominsoyl69a02b1
 Method BLASTX
 NCBI GI g2494034
 BLAST score 602
 E value 2.0e-62
 Match length 188
 % identity 62
 NCBI Description DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG KINASE 1) >gi_2129573_pir_S71467 diacylglycerol kinase - Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787) diacylglycerol kinase [Arabidopsis thaliana]

Seq. No. 26674
 Contig ID 142960_1.R1040
 5'-most EST jC-gmfl02220136b04a1
 Method BLASTX
 NCBI GI g2245004
 BLAST score 495
 E value 5.0e-50
 Match length 160
 % identity 57
 NCBI Description (Z97341) similarity to membrane transport protein [Arabidopsis thaliana]

Seq. No. 26675
 Contig ID 142966_1.R1040
 5'-most EST asn701139805.h1

Seq. No. 26676
 Contig ID 142994_1.R1040
 5'-most EST jC-gmro02910075e08a1

Seq. No. 26677
 Contig ID 142995_1.R1040

Method	BLASTX
NCBI GI	g1491710
BLAST score	125
E value	3.0e-10
Match length	65
% identity	41
NCBI Description	(X96506) alpha subunit; forms heterodimer with NC2 alpha/Dr1 [Homo sapiens]
Seq. No.	26685
Contig ID	143179_1.R1040
5'-most EST	jC-gmfl02220073g11a1
Seq. No.	26686
Contig ID	143238_1.R1040
5'-most EST	ncj700987731.h1
Seq. No.	26687
Contig ID	143253_1.R1040
5'-most EST	uC-gmrominsoyl11d06b1
Method	BLASTX
NCBI GI	g2501296
BLAST score	301
E value	4.0e-27
Match length	77
% identity	71
NCBI Description	DNA GYRASE SUBUNIT B >gi_1652801_dbj_BAA17720_ (D90908) DNA gyrase B subunit [Synechocystis sp.]
Seq. No.	26688
Contig ID	143259_1.R1040
5'-most EST	ncj700987765.h1
Seq. No.	26689
Contig ID	143278_1.R1040
5'-most EST	gsv701048101.h1
Seq. No.	26690
Contig ID	143278_3.R1040
5'-most EST	zzp700835694.h1
Seq. No.	26691
Contig ID	143286_1.R1040
5'-most EST	ncj700987804.h1
Method	BLASTX
NCBI GI	g4467111
BLAST score	333
E value	4.0e-31
Match length	99
% identity	66
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]
Seq. No.	26692
Contig ID	143291_1.R1040
5'-most EST	jC-gmst02400029g04a1
Method	BLASTN
NCBI GI	g166411

% identity 58
 NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 26699
 Contig ID 143463_1.R1040
 5'-most EST ncj700988163.h1
 Method BLASTN
 NCBI GI g16508
 BLAST score 75
 E value 4.0e-34
 Match length 147
 % identity 88
 NCBI Description A.thaliana DNA for S-adenosylmethionine synthetase gene
 sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana
 S-adenosylmethionine synthetase gene, complete cds

Seq. No. 26700
 Contig ID 143470_1.R1040
 5'-most EST zhf700955313.h1
 Method BLASTX
 NCBI GI g1495251
 BLAST score 565
 E value 2.0e-58
 Match length 124
 % identity 87
 NCBI Description (270314) heat-shock protein [Arabidopsis thaliana]

Seq. No. 26701
 Contig ID 143472_1.R1040
 5'-most EST zhf700952045.h1
 Method BLASTX
 NCBI GI g1172441
 BLAST score 163
 E value 7.0e-11
 Match length 48
 % identity 67
 NCBI Description POSSIBLE TRANSCRIPTION FACTOR POSF21 >gi_99685_pir__S21883
 DNA-binding protein POSF21 - Arabidopsis thaliana
 >gi_16429_emb_CAA43366_ (X61031) posF21 [Arabidopsis
 thaliana]

Seq. No. 26702
 Contig ID 143472_2.R1040
 5'-most EST smc700744982.h1

Seq. No. 26703
 Contig ID 143477_1.R1040
 5'-most EST sat701012012.h1

Seq. No. 26704
 Contig ID 143519_1.R1040
 5'-most EST ncj700988274.h1

Seq. No. 26705
 Contig ID 143520_1.R1040
 5'-most EST ncj700988275.h1
 Method BLASTX

NCBI GI g2832664
 BLAST score 214
 E value 1.0e-17
 Match length 73
 % identity 58
 NCBI Description (AL021710) pollen-specific protein - like [Arabidopsis thaliana]

Seq. No. 26706
 Contig ID 143582_1.R1040
 5'-most EST ncj700988393.h1
 Method BLASTX
 NCBI GI g4455278
 BLAST score 128
 E value 4.0e-10
 Match length 90
 % identity 43
 NCBI Description (AL035527) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26707
 Contig ID 143588_1.R1040
 5'-most EST uC-gmflminsoy075c09b1
 Method BLASTX
 NCBI GI g2660677
 BLAST score 722
 E value 2.0e-76
 Match length 251
 % identity 59
 NCBI Description (AC002342) unknown protein [Arabidopsis thaliana]

Seq. No. 26708
 Contig ID 143607_1.R1040
 5'-most EST uC-gmflminsoy035b02b1

Seq. No. 26709
 Contig ID 143621_1.R1040
 5'-most EST fC-gmle700871981f3
 Method BLASTX
 NCBI GI g2623300
 BLAST score 1045
 E value 1.0e-114
 Match length 372
 % identity 55
 NCBI Description (AC002409) putative protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 26710
 Contig ID 143639_1.R1040
 5'-most EST leu701147859.h1
 Method BLASTX
 NCBI GI g3510254
 BLAST score 227
 E value 8.0e-19
 Match length 81
 % identity 58
 NCBI Description (AC005310) putative zinc transporter [Arabidopsis thaliana]

Seq. No. 26711
 Contig ID 143649_1.R1040
 5'-most EST ncj700988522.h1

Seq. No. 26712
 Contig ID 143656_1.R1040
 5'-most EST ncj700988535.h1

Seq. No. 26713
 Contig ID 143658_1.R1040
 5'-most EST ncj700988541.h1

Seq. No. 26714
 Contig ID 143668_1.R1040
 5'-most EST ncj700988559.h1
 Method BLASTX
 NCBI GI g1169128
 BLAST score 228
 E value 1.0e-18
 Match length 111
 % identity 42
 NCBI Description SERINE/THREONINE-PROTEIN KINASE CTR1 >gi_166680 (L08789)
 protein kinase [Arabidopsis thaliana] >gi_166682 (L08790)
 protein kinase [Arabidopsis thaliana]

Seq. No. 26715
 Contig ID 143680_1.R1040
 5'-most EST jC-gmro02910016e12a1

Seq. No. 26716
 Contig ID 143730_1.R1040
 5'-most EST zhf700964905.h1

Seq. No. 26717
 Contig ID 143735_1.R1040
 5'-most EST ncj700988655.h1
 Method BLASTX
 NCBI GI g1245343
 BLAST score 242
 E value 2.0e-20
 Match length 76
 % identity 58
 NCBI Description (U50194) tripeptidylpeptidase II [Rattus norvegicus]

Seq. No. 26718
 Contig ID 143755_1.R1040
 5'-most EST gsv701044887.h1
 Method BLASTX
 NCBI GI g2160182
 BLAST score 345
 E value 2.0e-32
 Match length 104
 % identity 66
 NCBI Description (AC000132) ESTs gb_ATTS1236, gb_T43334, gb_N97019, gb_AA395203
 come from this gene. [Arabidopsis thaliana]

Seq. No. 26719

Contig ID 143765 1.R1040
 5'-most EST pst700645716.h1
 Method BLASTX
 NCBI GI g2245009
 BLAST score 201
 E value 7.0e-16
 Match length 54
 % identity 70
 NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26720
 Contig ID 143912 1.R1040
 5'-most EST txt700731337.h1

Seq. No. 26721
 Contig ID 143912 2.R1040
 5'-most EST zhf700958462.h1

Seq. No. 26722
 Contig ID 143936 1.R1040
 5'-most EST kl1701207242.h1

Seq. No. 26723
 Contig ID 143962 1.R1040
 5'-most EST txt700731496.h1
 Method BLASTX
 NCBI GI g1174718
 BLAST score 178
 E value 2.0e-13
 Match length 41
 % identity 83
 NCBI Description PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR
 >gi_322579_pir_JQ1674 receptor protein kinase TMK1 (EC
 2.7.1.-) precursor - Arabidopsis thaliana >gi_166888
 (L00670) protein kinase [Arabidopsis thaliana]

Seq. No. 26724
 Contig ID 144083 1.R1040
 5'-most EST kl1701202564.h1

Seq. No. 26725
 Contig ID 144117 1.R1040
 5'-most EST g5342789
 Method BLASTX
 NCBI GI g1705678
 BLAST score 364
 E value 1.0e-34
 Match length 108
 % identity 72
 NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
 PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213)
 valosin-containing protein [Glycine max]

Seq. No. 26726
 Contig ID 144139 2.R1040
 5'-most EST txt700731771.h1
 Method BLASTX

0364016100

0364016100

0364016100

0364016100

0364016100

0364016100

0364016100

0364016100

09684016-101000

Seq. No. 26767
Contig ID 144874 1.R1040
5'-most EST rca701002368.h1

Seq. No. 26768
Contig ID 144909 1.R1040
5'-most EST txt700733296.h1

Seq. No. 26769
Contig ID 144952 1.R1040
5'-most EST txt700733379.h1

Seq. No. 26770
Contig ID 144964 1.R1040
5'-most EST txt700733408.h1

Seq. No. 26771
Contig ID 145017 1.R1040
5'-most EST zsg701119121.h1
Method BLASTX
NCBI GI g3219269
BLAST score 279
E value 1.0e-48
Match length 117
% identity 81
NCBI Description (AB015314) MAP kinase kinase 3 [Arabidopsis thaliana]

Seq. No. 26772
Contig ID 145028 1.R1040
5'-most EST txt700733518.h1
Method BLASTX
NCBI GI g2880046
BLAST score 147
E value 2.0e-09
Match length 65
% identity 46
NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26773
Contig ID 145043 1.R1040
5'-most EST jC-gmfl02220078a05a1

Seq. No. 26774
Contig ID 145056 1.R1040
5'-most EST txt700737183.h1

Seq. No. 26775
Contig ID 145106 1.R1040
5'-most EST gsv701043865.h1

Seq. No. 26776
Contig ID 145110 1.R1040
5'-most EST g5126515
Method BLASTX
NCBI GI g2323410
BLAST score 994
E value 1.0e-108

gene; cDNA EST EMBL:D69055 comes from this gene; cDNA EST
EMBL:D64515 comes from this gene; cDNA EST EMBL:D655

Seq. No. 26791
Contig ID 145499_1.R1040
5'-most EST txt700734406.h1

Seq. No. 26792
Contig ID 145502_1.R1040
5'-most EST txt700734410.h1

Seq. No. 26793
Contig ID 145514_1.R1040
5'-most EST uC-gmrominsoy307f01b1
Method BLASTX
NCBI GI g3142291
BLAST score 487
E value 6.0e-49
Match length 167
% identity 54
NCBI Description (AC002411) Contains similarity to adenylate cyclase
gb_AF012921 from Magnaporthe grisea. EST gb_Z24512 comes
from this gene. [Arabidopsis thaliana]

Seq. No. 26794
Contig ID 145544_1.R1040
5'-most EST zpv700761035.h1
Method BLASTX
NCBI GI g4249416
BLAST score 291
E value 4.0e-26
Match length 89
% identity 58
NCBI Description (AC006072) putative exoribonuclease (also contains
zinc-finger C2H2-type domain) [Arabidopsis thaliana]

Seq. No. 26795
Contig ID 145570_1.R1040
5'-most EST dpv701101324.h1
Method BLASTX
NCBI GI g3377843
BLAST score 151
E value 6.0e-10
Match length 102
% identity 41
NCBI Description (AF076274) contains similarity to rat p47 protein
(GB:AB002086) [Arabidopsis thaliana]

Seq. No. 26796
Contig ID 145635_1.R1040
5'-most EST jC-gmro02910062d04a1
Method BLASTX
NCBI GI g2911042
BLAST score 682
E value 3.0e-89
Match length 226
% identity 79

NCBI Description (AL021961) Phosphoglycerate dehydrogenase - like protein
[Arabidopsis thaliana]

Seq. No. 26797
Contig ID 145698_1.R1040
5'-most EST gsv701055801.h1
Method BLASTX
NCBI GI g4218011
BLAST score 442
E value 6.0e-44
Match length 101
% identity 80
NCBI Description (AC006135) putative protein kinase [Arabidopsis thaliana]
>gi_4309721_gb_AAD15491_ (AC006439) putative
serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 26798
Contig ID 145700_1.R1040
5'-most EST pmv700888891.h1
Method BLASTX
NCBI GI g3132478
BLAST score 311
E value 1.0e-28
Match length 146
% identity 47
NCBI Description (AC003096) bZIP-like protein [Arabidopsis thaliana]

Seq. No. 26799
Contig ID 145704_1.R1040
5'-most EST jC-gmle01810066b02d1

Seq. No. 26800
Contig ID 145713_1.R1040
5'-most EST pmv700888646.h1

Seq. No. 26801
Contig ID 145743_1.R1040
5'-most EST crh700852487.h1
Method BLASTX
NCBI GI g2244996
BLAST score 262
E value 7.0e-37
Match length 131
% identity 59
NCBI Description (Z97341) similarity to a membrane-associated salt-inducible
protein [Arabidopsis thaliana]

Seq. No. 26802
Contig ID 145763_1.R1040
5'-most EST smc700746937.h1

Seq. No. 26803
Contig ID 145785_1.R1040
5'-most EST jC-gmst02400013e01a1

Seq. No. 26804
Contig ID 145786_1.R1040

5'-most EST smc700744318.h1
 Method BLASTX
 NCBI GI g3549667
 BLAST score 587
 E value 6.0e-61
 Match length 136
 % identity 85
 NCBI Description (AL031394) Arabidopsis dynamin-like protein ADL2
 [Arabidopsis thaliana]

Seq. No. 26805
 Contig ID 145799 1.R1040
 5'-most EST dpv701100879.h1

Seq. No. 26806
 Contig ID 145803 1.R1040
 5'-most EST txt700734949.h1

Seq. No. 26807
 Contig ID 145828 1.R1040
 5'-most EST pmv700893370.h1
 Method BLASTX
 NCBI GI g1169198
 BLAST score 267
 E value 2.0e-23
 Match length 92
 % identity 59
 NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR
 >gi_479738_pir_S35270 hypothetical protein - Arabidopsis
 thaliana >gi_166926 (L11367) [Arabidopsis thaliana
 unidentified mRNA sequence, complete cds.], gene product
 [Arabidopsis thaliana]

Seq. No. 26808
 Contig ID 145839 1.R1040
 5'-most EST awf700837802.h1
 Method BLASTX
 NCBI GI g3386597
 BLAST score 169
 E value 1.0e-11
 Match length 48
 % identity 71
 NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
 >gi_3702347 (AC005397) putative permease [Arabidopsis
 thaliana]

Seq. No. 26809
 Contig ID 145844 1.R1040
 5'-most EST kl1701202434.h1
 Method BLASTX
 NCBI GI g3452263
 BLAST score 435
 E value 4.0e-53
 Match length 133
 % identity 80
 NCBI Description (AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis
 thaliana]

Seq. No. 26810
 Contig ID 145846 1.R1040
 5'-most EST txt700735025.h1
 Method BLASTX
 NCBI GI g730934
 BLAST score 227
 E value 7.0e-19
 Match length 102
 % identity 46
 NCBI Description QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE
 TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)
 >gi_2137015_pir_S68430 queueine tRNA-ribosyltransferase (EC
 2.4.2.29), 60K chain - rabbit >gi_623547 (L37420) queueine
 tRNA-ribosyltransferase [Oryctolagus cuniculus]

Seq. No. 26811
 Contig ID 145866 1.R1040
 5'-most EST txt700735055.h1

Seq. No. 26812
 Contig ID 145873 1.R1040
 5'-most EST leu701153435.h1

Seq. No. 26813
 Contig ID 145884 1.R1040
 5'-most EST txt700735091.h1

Seq. No. 26814
 Contig ID 145929 1.R1040
 5'-most EST txt700735202.h1
 Method BLASTX
 NCBI GI g2494174
 BLAST score 444
 E value 3.0e-60
 Match length 180
 % identity 67
 NCBI Description GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi_497979 (U10034)
 glutamate decarboxylase [Arabidopsis thaliana]

Seq. No. 26815
 Contig ID 145967 1.R1040
 5'-most EST pxt700944894.h1

Seq. No. 26816
 Contig ID 146045 1.R1040
 5'-most EST txt700735414.h1

Seq. No. 26817
 Contig ID 146091 1.R1040
 5'-most EST txt700735488.h1

Seq. No. 26818
 Contig ID 146129 1.R1040
 5'-most EST txt700735551.h1
 Method BLASTX
 NCBI GI g440965

E value	8.0e-22
Match length	86
% identity	17
NCBI Description	(Y12781) transducin (beta) like 1 protein [Homo sapiens]
Seq. No.	26827
Contig ID	146248_1.R1040
5'-most EST	uC-gmropic104f07b1
Seq. No.	26828
Contig ID	146258_1.R1040
5'-most EST	txt700735801.h1
Seq. No.	26829
Contig ID	146261_1.R1040
5'-most EST	uC-gmrominsoy086c07b1
Seq. No.	26830
Contig ID	146338_1.R1040
5'-most EST	jsh701067558.h1
Seq. No.	26831
Contig ID	146351_1.R1040
5'-most EST	txt700735962.h1
Seq. No.	26832
Contig ID	146360_1.R1040
5'-most EST	txt700735975.h1
Method	BLASTX
NCBI GI	g3386604
BLAST score	322
E value	3.0e-30
Match length	82
% identity	76
NCBI Description	(AC004665) putative protein kinase [Arabidopsis thaliana]
Seq. No.	26833
Contig ID	146411_1.R1040
5'-most EST	fua701040350.h1
Seq. No.	26834
Contig ID	146414_1.R1040
5'-most EST	k11701214317.h1
Method	BLASTX
NCBI GI	g3746064
BLAST score	145
E value	6.0e-09
Match length	45
% identity	56
NCBI Description	(AC005311) unknown protein [Arabidopsis thaliana]
Seq. No.	26835
Contig ID	146423_1.R1040
5'-most EST	uC-gmflminsoy010g10b1
Method	BLASTX
NCBI GI	g4091810
BLAST score	204

E value 9.0e-16
 Match length 112
 % identity 54
 NCBI Description (AF053345) fatty acid elongase 3-ketoacyl-CoA synthase 1
 [Arabidopsis thaliana]

Seq. No. 26836
 Contig ID 146450 1.R1040
 5'-most EST txt700736183.h1
 Method BLASTX
 NCBI GI g1707945
 BLAST score 295
 E value 4.0e-27
 Match length 81
 % identity 69
 NCBI Description GLYCOGEN OPERON PROTEIN GLGX HOMOLOG
 >gi_1403478_emb_CAA98327_ (Z74020) glgX [Mycobacterium
 tuberculosis]

Seq. No. 26837
 Contig ID 146452 1.R1040
 5'-most EST epx701108278.h1

Seq. No. 26838
 Contig ID 146456 1.R1040
 5'-most EST txt700736189.h1

Seq. No. 26839
 Contig ID 146502 1.R1040
 5'-most EST hrw701062412.h1

Seq. No. 26840
 Contig ID 146531 2.R1040
 5'-most EST uC-gmropic107e10b1

Seq. No. 26841
 Contig ID 146538 1.R1040
 5'-most EST txt700736335.h1

Seq. No. 26842
 Contig ID 146599 1.R1040
 5'-most EST txt700736452.h1
 Method BLASTX
 NCBI GI g3850587
 BLAST score 212
 E value 4.0e-17
 Match length 86
 % identity 52
 NCBI Description (AC005278) Strong similarity to gi_2244780 hypothetical
 protein from Arabidopsis thaliana Chromosome 4 contig
 gb_297335. [Arabidopsis thaliana]

Seq. No. 26843
 Contig ID 146647 1.R1040
 5'-most EST jC-gmfl02220132ab10d1

Seq. No. 26844

0664018-101000

NCBI Description P1LZ02 PROTEIN >gi_99973_pir_S11881 hypothetical protein
(clone pP1LZ2) - large-leaved lupine >gi_19507_emb_CAA36069_
(X51767) put. pP1LZ2 product (AA 1-164) [Lupinus
polyphyllus]

```
Seq. No.          26881
Contig ID         147420_1.R1040
5'-most EST      wrg700786058.h2
Method            BLASTX
NCBI GI           g3776025
BLAST score       410
E value           2.0e-40
Match length      97
% identity        78
NCBI Description  (AJ010474) RNA helicase [Arabidopsis thaliana]
```

Seq. No.	26883
Contig ID	147468_1.R1040
5'-most EST	asn701136493.h1

```
Seq. No.                26884
Contig ID               147499_1.R1040
5'-most EST            zhf700958443.h1
Method                  BLASTX
NCBI GI                 g4455131
BLAST score             224
E value                 3.0e-18
Match length            132
```


0963401611000

NCBI Description (AF053702) hypothetical protein [Mesembryanthemum crystallinum]

NCBI Description (AF080567) pullulanase-type starch debranching enzyme [Zea mays]

NCBI Description (AC006068) putative glycogenin-2 protein [Arabidopsis thaliana]

NCBI Description HIGH AFFINITY AMMONIUM TRANSPORTER >gi_551219_emb_CAA53473_ (X75879) amt1 [Arabidopsis thaliana]

Seq. No.	26889
Contig ID	147626_1.R1040
5'-most EST	wrg700786484.h1

Seq. No. 26890

% identity	98
NCBI Description	Corn 22 kDa zein protein gene, complete cds
Seq. No.	26898
Contig ID	147740_1.R1040
5'-most EST	leu701154242.h1
Seq. No.	26899
Contig ID	147753_1.R1040
5'-most EST	wrg700788061.h1
Seq. No.	26900
Contig ID	147765_1.R1040
5'-most EST	wrg700786754.h2
Seq. No.	26901
Contig ID	147792_1.R1040
5'-most EST	wrg700786840.h2
Method	BLASTN
NCBI GI	g168681
BLAST score	243
E value	1.0e-134
Match length	259
% identity	98
NCBI Description	Maize 19 kDa zein mRNA, clone cZ19D1, complete cds. >gi_270686_gb_I03333_ Sequence 8 from Patent US
Seq. No.	26902
Contig ID	147793_1.R1040
5'-most EST	wrg700786793.h2
Seq. No.	26903
Contig ID	147803_1.R1040
5'-most EST	fC-gmro7000747078r1
Method	BLASTX
NCBI GI	g4432846
BLAST score	372
E value	2.0e-35
Match length	121
% identity	64
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.	26904
Contig ID	147821_1.R1040
5'-most EST	wrg700786834.h2
Seq. No.	26905
Contig ID	147832_1.R1040
5'-most EST	jC-gmst02400039h12a1
Seq. No.	26906
Contig ID	147887_1.R1040
5'-most EST	wrg700786944.h2
Seq. No.	26907
Contig ID	147887_2.R1040
5'-most EST	smc700744330.h1

NCBI GI g4567279
 BLAST score 432
 E value 1.0e-42
 Match length 105
 % identity 74
 NCBI Description (AC006841) putative serine/threonine protein kinase
 [Arabidopsis thaliana]

Seq. No. 26922
 Contig ID 148088 1.R1040
 5'-most EST jC-gmfl02220148c07a1

Seq. No. 26923
 Contig ID 148091 1.R1040
 5'-most EST g5127006
 Method BLASTX
 NCBI GI g2160161
 BLAST score 207
 E value 5.0e-16
 Match length 162
 % identity 11
 NCBI Description (AC000132) F21M12.7 gene product [Arabidopsis thaliana]

Seq. No. 26924
 Contig ID 148098 1.R1040
 5'-most EST xzm700763723.h1
 Method BLASTN
 NCBI GI g3493646
 BLAST score 79
 E value 3.0e-36
 Match length 187
 % identity 86
 NCBI Description Pimpinella brachycarpa transcription activator (MADS1)
 mRNA, complete cds

Seq. No. 26925
 Contig ID 148177 1.R1040
 5'-most EST zzp700829984.h1
 Method BLASTX
 NCBI GI g2194142
 BLAST score 259
 E value 4.0e-22
 Match length 112
 % identity 47
 NCBI Description (AC002062) ESTs gb_N38288, gb_T43486, gb_AA395242 come from
 this gene. [Arabidopsis thaliana]

Seq. No. 26926
 Contig ID 148184 1.R1040
 5'-most EST wrq700787429.h2

Seq. No. 26927
 Contig ID 148191 1.R1040
 5'-most EST g5606337
 Method BLASTX
 NCBI GI g4432846
 BLAST score 398

E value 3.0e-56
 Match length 268
 % identity 47
 NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 26928
 Contig ID 148193_1.R1040
 5'-most EST g5607183
 Method BLASTX
 NCBI GI g1084301
 BLAST score 684
 E value 4.0e-72
 Match length 172
 % identity 81
 NCBI Description pyruvate,orthophosphate dikinase (EC 2.7.9.1) - common ice
 plant >gi_559471_emb_CAA55143_ (X78347)
 pyruvate,orthophosphate dikinase [Mesembryanthemum
 crystallinum]

Seq. No. 26929
 Contig ID 148203_1.R1040
 5'-most EST wrg700787450.h2
 Method BLASTX
 NCBI GI g4538911
 BLAST score 151
 E value 3.0e-22
 Match length 85
 % identity 67
 NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No. 26930
 Contig ID 148206_1.R1040
 5'-most EST wrg700787453.h2
 Method BLASTX
 NCBI GI g2499989
 BLAST score 144
 E value 3.0e-09
 Match length 85
 % identity 39
 NCBI Description PEPTIDYL-TRNA HYDROLASE (PTH) >gi_1001232_dbj_BAA10473_
 (D64003) peptidyl-tRNA hydrolase [Synechocystis sp.]

Seq. No. 26931
 Contig ID 148220_1.R1040
 5'-most EST g5509244
 Method BLASTX
 NCBI GI g1001253
 BLAST score 241
 E value 4.0e-20
 Match length 140
 % identity 41
 NCBI Description (D64003) hypothetical protein [Synechocystis sp.]

Seq. No. 26932
 Contig ID 148254_1.R1040
 5'-most EST zhf700956404.h1

09684015.101000

Method	BLASTX
NCBI GI	g3004655
BLAST score	327
E value	2.0e-30
Match length	140
% identity	52
NCBI Description	(AF017777) waclaw [Drosophila melanogaster]
Seq. No.	26965
Contig ID	148629_1.R1040
5'-most EST	wrg700788056.h1
Seq. No.	26966
Contig ID	148632_1.R1040
5'-most EST	all1700863205.h1
Seq. No.	26967
Contig ID	148660_1.R1040
5'-most EST	g4291611
Seq. No.	26968
Contig ID	148697_1.R1040
5'-most EST	wrg700788214.h1
Seq. No.	26969
Contig ID	148720_1.R1040
5'-most EST	fua701038872.h1
Seq. No.	26970
Contig ID	148721_1.R1040
5'-most EST	gsv701051145.h1
Method	BLASTX
NCBI GI	g461729
BLAST score	251
E value	8.0e-22
Match length	63
% identity	75
NCBI Description	10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) >gi_2146744_pir_S65597 probable chaperonin, 10K - Arabidopsis thaliana >gi_166662 (L02843) 10 kDa chaperonin [Arabidopsis thaliana]
Seq. No.	26971
Contig ID	148780_1.R1040
5'-most EST	wrg700788389.h1
Method	BLASTX
NCBI GI	g2264382
BLAST score	257
E value	2.0e-22
Match length	79
% identity	58
NCBI Description	(AC002354) putative tetracycline transporter-like protein [Arabidopsis thaliana]
Seq. No.	26972
Contig ID	148827_1.R1040
5'-most EST	leu701152971.h1

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0	00000000	00000001	00000002	00000003	00000004	00000005	00000006	00000007	00000008	00000009	0000000A	0000000B	0000000C	0000000D	0000000E	0000000F	00000000	00000010	00000011	00000012	00000013	00000014	00000015	00000016	00000017	00000018	00000019	0000001A	0000001B	0000001C	0000001D	0000001E	0000001F	00000020	00000021	00000022	00000023	00000024	00000025	00000026	00000027	00000028	00000029	0000002A	0000002B	0000002C	0000002D	0000002E	0000002F	00000030	00000031	00000032	00000033	00000034	00000035	00000036	00000037	00000038	00000039	0000003A	0000003B	0000003C	0000003D	0000003E	0000003F	00000040	00000041	00000042	00000043	00000044	00000045	00000046	00000047	00000048	00000049	0000004A	0000004B	0000004C	0000004D	0000004E	0000004F	00000050	00000051	00000052	00000053	00000054	00000055	00000056	00000057	00000058	00000059	0000005A	0000005B	0000005C	0000005D	0000005E	0000005F	00000060	00000061	00000062	00000063	00000064	00000065	00000066	00000067	00000068	00000069	0000006A	0000006B	0000006C	0000006D	0000006E	0000006F	00000070	00000071	00000072	00000073	00000074	00000075	00000076	00000077	00000078	00000079	0000007A	0000007B	0000007C	0000007D	0000007E	0000007F	00000080	00000081	00000082	00000083	00000084	00000085	00000086	00000087	00000088	00000089	0000008A	0000008B	0000008C	0000008D	0000008E	0000008F	00000090	00000091	00000092	00000093	00000094	00000095	00000096	00000097	00000098	00000099	0000009A	0000009B	0000009C	0000009D	0000009E	0000009F	000000A0	000000A1	000000A2	000000A3	000000A4	000000A5	000000A6	000000A7	000000A8	000000A9	000000AA	000000AB	000000AC	000000AD	000000AE	000000AF	000000B0	000000B1	000000B2	000000B3	000000B4	000000B5	000000B6	000000B7	000000B8	000000B9	000000BA	000000BB	000000BC	000000BD	000000BE	000000BF	000000C0	000000C1	000000C2	000000C3	000000C4	000000C5	000000C6	000000C7	000000C8	000000C9	000000CA	000000CB	000000CC	000000CD	000000CE	000000CF	000000D0	000000D1	000000D2	000000D3	000000D4	000000D5	000000D6	000000D7	000000D8	000000D9	000000DA	000000DB	000000DC	000000DD	000000DE	000000DF	000000E0	000000E1	000000E2	000000E3	000000E4	000000E5	000000E6	000000E7	000000E8	000000E9	000000EA	000000EB	000000EC	000000ED	000000EE	000000EF	000000F0	000000F1	000000F2	000000F3	000000F4	000000F5	000000F6	000000F7	000000F8	000000F9	000000FA	000000FB	000000FC	000000FD	000000FE	000000FF	00000100	00000101	00000102	00000103	00000104

Seq. No. 26983

5'-most EST hrw701061007.h1
 Seq. No. 27000
 Contig ID 149204_2.R1040
 5'-most EST uC-gmronoir015d09b1

Seq. No. 27001
 Contig ID 149219_1.R1040
 5'-most EST uC-gmropic092b12b1

Seq. No. 27002
 Contig ID 149228_1.R1040
 5'-most EST zhf700956157.h1
 Method BLASTX
 NCBI GI g4314357
 BLAST score 262
 E value 9.0e-23
 Match length 153
 % identity 32
 NCBI Description (AC006340) putative nucleic acid binding protein
 [Arabidopsis thaliana]

Seq. No. 27003
 Contig ID 149229_1.R1040
 5'-most EST uC-gmflminsoy046f04b1
 Method BLASTX
 NCBI GI g4567227
 BLAST score 581
 E value 5.0e-60
 Match length 197
 % identity 60
 NCBI Description (AC007119) putative transport protein [Arabidopsis
 thaliana]

Seq. No. 27004
 Contig ID 149246_1.R1040
 5'-most EST wrq700789354.h2

Seq. No. 27005
 Contig ID 149248_1.R1040
 5'-most EST rca701001671.h1
 Method BLASTX
 NCBI GI g437327
 BLAST score 689
 E value 2.0e-72
 Match length 130
 % identity 94
 NCBI Description (L04497) MYB A; putative [Gossypium hirsutum]

Seq. No. 27006
 Contig ID 149250_1.R1040
 5'-most EST uC-gmflminsoy012a03b1
 Method BLASTN
 NCBI GI g1218003
 BLAST score 184
 E value 5.0e-99
 Match length 391

% identity 87
NCBI Description Glycine max dynamin-like protein SDL5A mRNA, complete cds

Seq. No. 27007
Contig ID 149281_1.R1040
5'-most EST crh700854590.h1
Method BLASTX
NCBI GI g2980777
BLAST score 262
E value 7.0e-23
Match length 123
% identity 45
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 27008
Contig ID 149293_1.R1040
5'-most EST zzp700831677.h1

Seq. No. 27009
Contig ID 149296_1.R1040
5'-most EST fde700875241.h1
Method BLASTX
NCBI GI g2435517
BLAST score 319
E value 7.0e-30
Match length 84
% identity 68
NCBI Description (AF024504) contains similarity to peptidase family A1 [Arabidopsis thaliana]

Seq. No. 27010
Contig ID 149333_1.R1040
5'-most EST wrg700789476.h2

Seq. No. 27011
Contig ID 149339_1.R1040
5'-most EST bth700843894.h1
Method BLASTX
NCBI GI g2129918
BLAST score 149
E value 5.0e-10
Match length 62
% identity 53
NCBI Description BPF-1 protein - parsley >gi_396197_emb_CAA48413_ (X68337)
BPF-1 [Petroselinum crispum] >gi_441310_emb_CAA44518_
(X62653) BPF-1 [Petroselinum crispum]

Seq. No. 27012
Contig ID 149342_1.R1040
5'-most EST kl1701204637.h1
Method BLASTX
NCBI GI g2809246
BLAST score 260
E value 8.0e-23
Match length 70
% identity 67
NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana]

Seq. No. 27019
 Contig ID 149413 1.R1040
 5'-most EST wrg700789585.h2

Seq. No. 27020
 Contig ID 149425 1.R1040
 5'-most EST zhf700961927.h1
 Method BLASTX
 NCBI GI g2369714
 BLAST score 633
 E value 5.0e-66
 Match length 186
 % identity 71
 NCBI Description (297178) elongation factor 2 [Beta vulgaris]

Seq. No. 27021
 Contig ID 149425 2.R1040
 5'-most EST leu701146156.h1
 Method BLASTX
 NCBI GI g2369714
 BLAST score 138
 E value 1.0e-10
 Match length 50
 % identity 82
 NCBI Description (297178) elongation factor 2 [Beta vulgaris]

Seq. No. 27022
 Contig ID 149450 1.R1040
 5'-most EST wrg700789631.h2
 Method BLASTN
 NCBI GI g3985958
 BLAST score 50
 E value 3.0e-19
 Match length 170
 % identity 82
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No. 27023
 Contig ID 149458 1.R1040
 5'-most EST wrg700789641.h2

Seq. No. 27024
 Contig ID 149462 1.R1040
 5'-most EST jC-gmlé01810087b04a1
 Method BLASTX
 NCBI GI g476961
 BLAST score 586
 E value 1.0e-60
 Match length 167
 % identity 71
 NCBI Description chromodomain-helicase-DNA-binding protein, CHD-1 - mouse

Seq. No. 27025
 Contig ID 149470 1.R1040
 5'-most EST vzy700755452.h1

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Contig ID 149817 1.R1040
 5'-most EST g5752548
 Method BLASTX
 NCBI GI g3757520
 BLAST score 174
 E value 2.0e-12
 Match length 142
 % identity 40
 NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 27045
 Contig ID 149844 1.R1040
 5'-most EST wrg700790274.h2
 Method BLASTN
 NCBI GI g2293111
 BLAST score 165
 E value 1.0e-87
 Match length 456
 % identity 84
 NCBI Description V.faba mRNA for potassium channel

Seq. No. 27046
 Contig ID 149871 1.R1040
 5'-most EST wrg700790603.h2
 Method BLASTX
 NCBI GI g498038
 BLAST score 303
 E value 5.0e-28
 Match length 82
 % identity 63
 NCBI Description (L33792) lipid transfer protein [Senecio odorus]

Seq. No. 27047
 Contig ID 149877 1.R1040
 5'-most EST wrg700790319.h2

Seq. No. 27048
 Contig ID 149882 1.R1040
 5'-most EST wrg700790324.h2

Seq. No. 27049
 Contig ID 149883 1.R1040
 5'-most EST wrg700790325.h2

Seq. No. 27050
 Contig ID 149889 1.R1040
 5'-most EST wrg700790435.h2

Seq. No. 27051
 Contig ID 149893 1.R1040
 5'-most EST gsv701049523.h1

Seq. No. 27052
 Contig ID 149911 1.R1040
 5'-most EST rca701001536.h1
 Method BLASTX
 NCBI GI g3738298

5'-most EST wrg700790636.h2
 Method BLASTX
 NCBI GI g2854049
 BLAST score 148
 E value 3.0e-09
 Match length 80
 % identity 39
 NCBI Description (AF044260) receptor serine/threonine kinase; protein kinase [Oryza sativa]

Seq. No. 27059
 Contig ID 149933_1.R1040
 5'-most EST zh700953875.h1
 Method BLASTX
 NCBI GI g4508077
 BLAST score 213
 E value 3.0e-17
 Match length 73
 % identity 59
 NCBI Description (AC005882) 62114 [Arabidopsis thaliana]

Seq. No. 27060
 Contig ID 149965_1.R1040
 5'-most EST ep701104103.h1
 Method BLASTX
 NCBI GI g2961384
 BLAST score 169
 E value 4.0e-12
 Match length 83
 % identity 35
 NCBI Description (AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]

Seq. No. 27061
 Contig ID 149975_1.R1040
 5'-most EST zzp700829909.h1
 Method BLASTX
 NCBI GI g2947062
 BLAST score 144
 E value 2.0e-09
 Match length 66
 % identity 56
 NCBI Description (AC002521) unknown protein [Arabidopsis thaliana]

Seq. No. 27062
 Contig ID 150015_1.R1040
 5'-most EST fde700875304.h1
 Method BLASTX
 NCBI GI g3005983
 BLAST score 461
 E value 2.0e-46
 Match length 104
 % identity 84
 NCBI Description (Y14387) lycopene epsilon-cyclase [Lycopersicon esculentum]

Seq. No. 27063
 Contig ID 150033_1.R1040

5'-most EST wrg700790543.h2

Seq. No. 27064
Contig ID 150050_1.R1040
5'-most EST wrg700790567.h2

Seq. No. 27065
Contig ID 150086_1.R1040
5'-most EST wrg700790621.h2
Method BLASTX
NCBI GI g4432848
BLAST score 158
E value 7.0e-19
Match length 80
% identity 74
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No. 27066
Contig ID 150098_1.R1040
5'-most EST wrg700790641.h2

Seq. No. 27067
Contig ID 150118_1.R1040
5'-most EST rca700997004.h1
Method BLASTX
NCBI GI g3914239
BLAST score 209
E value 1.0e-16
Match length 73
% identity 53
NCBI Description PROTEIN PHOSPHATASE 2C ABI2 (PP2C)
>gi_1945140_emb_CAA70163_(Y08966) ABI2 protein phosphatase
2C [Arabidopsis thaliana] >gi_1945142_emb_CAA70162_
(Y08965) ABI2 protein phosphatase 2C [Arabidopsis thaliana]
>gi_2564213_emb_CAA72538_(Y11840) ABI2 [Arabidopsis
thaliana]

Seq. No. 27068
Contig ID 150131_1.R1040
5'-most EST jC-gmst02400006b05a1

Seq. No. 27069
Contig ID 150138_1.R1040
5'-most EST sat701014816.h1

Seq. No. 27070
Contig ID 150146_1.R1040
5'-most EST wrg700790712.h1
Method BLASTX
NCBI GI g1167982
BLAST score 689
E value 3.0e-76
Match length 266
% identity 57
NCBI Description (U43892) ABC transporter-7 [Mus musculus]

Seq. No. 27071

Contig ID 150151 1.R1040
 5'-most EST jex700904456.h1
 Method BLASTN
 NCBI GI g534971
 BLAST score 251
 E value 1.0e-139
 Match length 419
 % identity 90
 NCBI Description V.faba (var. minor) mRNA for alpha 1,4-glucan phosphorylase L isoform

Seq. No. 27072
 Contig ID 150178 1.R1040
 5'-most EST jC-gmf102220080g02a1
 Method BLASTX
 NCBI GI g2773249
 BLAST score 175
 E value 2.0e-12
 Match length 77
 % identity 45
 NCBI Description (AF039707) glutamate carboxypeptidase II [Rattus norvegicus]

Seq. No. 27073
 Contig ID 150181 1.R1040
 5'-most EST wrg700790777.h1
 Method BLASTX
 NCBI GI g4262186
 BLAST score 515
 E value 3.0e-52
 Match length 125
 % identity 77
 NCBI Description (AC005508) Highly similar to cullin 3 [Arabidopsis thaliana]

Seq. No. 27074
 Contig ID 150183 1.R1040
 5'-most EST bth700846128.h1

Seq. No. 27075
 Contig ID 150245 1.R1040
 5'-most EST wrg700790893.h1
 Method BLASTX
 NCBI GI g2618689
 BLAST score 362
 E value 2.0e-34
 Match length 106
 % identity 74
 NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 27076
 Contig ID 150246 1.R1040
 5'-most EST wrg700790894.h1

Seq. No. 27077
 Contig ID 150272 1.R1040
 5'-most EST wrg700791278.h1

Seq. No. 27078
Contig ID 150285_1.R1040
5'-most EST wrg700790970.h1

Seq. No. 27079
Contig ID 150293_1.R1040
5'-most EST epx701107494.h1

Seq. No. 27080
Contig ID 150313_1.R1040
5'-most EST uC-gmronoir064g02b1

Seq. No. 27081
Contig ID 150335_1.R1040
5'-most EST zsg701118364.h1

Seq. No. 27082
Contig ID 150338_1.R1040
5'-most EST wrg700791052.h1
Method BLASTX
NCBI GI g3420054
BLAST score 173
E value 1.0e-12
Match length 78
% identity 45
NCBI Description (AC004680) unknown protein [Arabidopsis thaliana]

Seq. No. 27083
Contig ID 150352_1.R1040
5'-most EST wrg700791071.h1
Method BLASTX
NCBI GI g2674203
BLAST score 444
E value 2.0e-44
Match length 96
% identity 92
NCBI Description (AF036328) CLP protease regulatory subunit CLPX [Arabidopsis thaliana]

Seq. No. 27084
Contig ID 150363_1.R1040
5'-most EST eep700868248.h1

Seq. No. 27085
Contig ID 150365_1.R1040
5'-most EST g5677813

Seq. No. 27086
Contig ID 150377_1.R1040
5'-most EST g5342507

Seq. No. 27087
Contig ID 150380_1.R1040
5'-most EST wrg700791131.h1

Seq. No. 27088

NCBI GI g3135611
BLAST score 354
E value 1.0e-33
Match length 109
% identity 62
NCBI Description (AF062485) cellulose synthase [Arabidopsis thaliana]

Seq. No. 27095
Contig ID 150477_1.R1040
5'-most EST jC-gmle01810091g09a1
Method BLASTX
NCBI GI g2398831
BLAST score 392
E value 8.0e-38
Match length 213
% identity 43
NCBI Description (X75542) 4-coumarate:CoA ligase [Vanilla planifolia]

Seq. No. 27096
Contig ID 150525_1.R1040
5'-most EST wrq700791515.h1

Seq. No. 27097
Contig ID 150529_1.R1040
5'-most EST wrq700791520.h1

Seq. No. 27098
Contig ID 150562_1.R1040
5'-most EST rca700999075.h1
Method BLASTX
NCBI GI g3096949
BLAST score 262
E value 4.0e-34
Match length 88
% identity 74
NCBI Description (Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana]

Seq. No. 27099
Contig ID 150583_1.R1040
5'-most EST jsh701068834.h1

Seq. No. 27100
Contig ID 150617_1.R1040
5'-most EST wrq700791687.h1
Method BLASTX
NCBI GI g2864610
BLAST score 168
E value 6.0e-12
Match length 45
% identity 64
NCBI Description (AL021811) putative protein [Arabidopsis thaliana] >gi_4049336_emb_CAA22561_ (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 27101

Contig ID 150635_1.R1040
 5'-most EST pxt700944468.h1
 Method BLASTX
 NCBI GI g2117620
 BLAST score 447
 E value 2.0e-44
 Match length 101
 % identity 86
 NCBI Description peroxidase (EC 1.11.1.7) 1A - alfalfa
 >gi_971558_emb_CAA62225_ (X90692) peroxidase1A [Medicago
 sativa]

Seq. No. 27102
 Contig ID 150638_1.R1040
 5'-most EST leu701149501.h1

Seq. No. 27103
 Contig ID 150641_1.R1040
 5'-most EST smc700745926.h1

Seq. No. 27104
 Contig ID 150666_1.R1040
 5'-most EST vzy700755518.h1
 Method BLASTX
 NCBI GI g2129609
 BLAST score 284
 E value 1.0e-25
 Match length 82
 % identity 70
 NCBI Description HD-ZIP protein - Arabidopsis thaliana
 >gi_1212757_emb_CAA91183_ (Z54356) HD-ZIP [Arabidopsis
 thaliana]

Seq. No. 27105
 Contig ID 150677_1.R1040
 5'-most EST wrg700791793.h1
 Method BLASTN
 NCBI GI g4115338
 BLAST score 104
 E value 2.0e-51
 Match length 207
 % identity 26
 NCBI Description Pisum sativum (Alaska) ubiquitin (PUB4) gene, complete cds

Seq. No. 27106
 Contig ID 150699_1.R1040
 5'-most EST jC-gmle01810088h12a1
 Method BLASTX
 NCBI GI g1169586
 BLAST score 184
 E value 7.0e-14
 Match length 39
 % identity 90
 NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC
 (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
 (CY-F1) >gi_542079_pir_S41287 fructose-bisphosphatase (EC
 3.1.3.11) - potato >gi_440591_emb_CAA54265_ (X76946)

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Seq. No.          27108
Contig ID         150715_1.R1040
5'-most EST      rca701002482.h1
Method            BLASTX
NCBI GI           g2673918
BLAST score       403
E value           4.0e-39
Match length      96
% identity        77
NCBI Description  (AC002561) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.          27109
Contig ID         150721_1.R1040
5'-most EST      kmv700743705.h1
Method            BLASTX
NCBI GI           g2443350
BLAST score       172
E value           3.0e-19
Match length      95
% identity        53
NCBI Description  (AB001380) cytochrome P450 [Glycyrrhiza echinata]
```

```
Seq. No.          27110
Contig ID         150726_1.R1040
5'-most EST      wrg700791890.h1
Method            BLASTX
NCBI GI           g3176714
BLAST score       464
E value           3.0e-46
Match length      117
% identity        74
NCBI Description  (AC002392) putative tRNA-splicing endonuclease positive
                  effector [Arabidopsis thaliana]
```

```
Seq. No.          27111
Contig ID         150738_1.R1040
5'-most EST      wrg700792261.h1
Method            BLASTX
NCBI GI           g3461813
BLAST score       279
E value           3.0e-25
Match length      83
% identity        64
NCBI Description  (AC004138) putative sucrose/H+ symporter [Arabidopsis
                  thaliana]
```

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Contig ID	150828_1.R1040
5'-most EST	kl1701207943.h1
Seq. No.	27121
Contig ID	150830_1.R1040
5'-most EST	jc-gmst02400051b01a1
Method	BLASTX
NCBI GI	g2443887
BLAST score	911
E value	2.0e-98
Match length	285
% identity	65
NCBI Description	(AC002294) Similar to transcription factor qb_246606_1658307 and others [Arabidopsis thaliana]
Seq. No.	27122
Contig ID	150851_1.R1040
5'-most EST	gsv701056442.h1
Seq. No.	27123
Contig ID	150868_1.R1040
5'-most EST	wrg700792214.h1
Seq. No.	27124
Contig ID	150869_1.R1040
5'-most EST	fde700875090.h1
Method	BLASTX
NCBI GI	g3600059
BLAST score	367
E value	3.0e-35
Match length	103
% identity	62
NCBI Description	(AF080120) contains similarity to WB domains, G-beta repeats (Pfam: G-beta.hmm, score: 14.83 and 23.03) [Arabidopsis thaliana]
Seq. No.	27125
Contig ID	150893_2.R1040
5'-most EST	hrw701059939.h1
Seq. No.	27126
Contig ID	150914_1.R1040
5'-most EST	kl1701214979.h1
Seq. No.	27127
Contig ID	150927_1.R1040
5'-most EST	pcp700988714.h1
Seq. No.	27128
Contig ID	150946_1.R1040
5'-most EST	pcp700988754.h1
Seq. No.	27129
Contig ID	150949_1.R1040
5'-most EST	pcp700990760.h1
Method	BLASTX
NCBI GI	g3135269

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Match length	81
% identity	54
NCBI Description	(AF055848) subtilisin-like protease [Arabidopsis thaliana]
Seq. No.	27152
Contig ID	151087 1.R1040
5'-most EST	pcp700991071.h1
Seq. No.	27153
Contig ID	151095 1.R1040
5'-most EST	pcp700991080.h1
Seq. No.	27154
Contig ID	151127 1.R1040
5'-most EST	pcp700989157.h1
Method	BLASTX
NCBI GI	g2660670
BLAST score	469
E value	7.0e-48
Match length	117
% identity	83
NCBI Description	(AC002342) putative Cu ²⁺ -transporting ATPase [Arabidopsis thaliana]
Seq. No.	27155
Contig ID	151135 1.R1040
5'-most EST	fde700875359.h1
Method	BLASTX
NCBI GI	g4468804
BLAST score	178
E value	4.0e-13
Match length	108
% identity	23
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]
Seq. No.	27156
Contig ID	151152 1.R1040
5'-most EST	kl1701214981.h1
Method	BLASTX
NCBI GI	g283966
BLAST score	590
E value	6.0e-61
Match length	173
% identity	67
NCBI Description	activator 1 37K chain - human
Seq. No.	27157
Contig ID	151161 1.R1040
5'-most EST	pcp700989236.h1
Seq. No.	27158
Contig ID	151183 1.R1040
5'-most EST	zsg701122867.h1
Method	BLASTN
NCBI GI	g1396053
BLAST score	272
E value	1.0e-151

% identity 43
 NCBI Description (AC006340) putative copia-like retrotransposon Hopscotch
 [Arabidopsis thaliana]

Seq. No. 27222
 Contig ID 152182_1.R1040
 5'-most EST kll1701204629.h1
 Method BLASTN
 NCBI GI g3868723
 BLAST score 73
 E value 1.0e-32
 Match length 412
 % identity 84

NCBI Description Arabidopsis thaliana chromosome V map 60.5 cM, complete
 sequence [Arabidopsis thaliana]

Seq. No. 27223
 Contig ID 152226_1.R1040
 5'-most EST kll1701214119.h1

Seq. No. 27224
 Contig ID 152229_1.R1040
 5'-most EST pcp700991187.h1

Seq. No. 27225
 Contig ID 152236_1.R1040
 5'-most EST pcp700991196.h1
 Method BLASTX
 NCBI GI g4218062
 BLAST score 250
 E value 1.0e-21
 Match length 115
 % identity 41
 NCBI Description (AB015906) actin-related protein [Homo sapiens]

Seq. No. 27226
 Contig ID 152238_1.R1040
 5'-most EST uC-gmropic036h09b1

Seq. No. 27227
 Contig ID 152253_1.R1040
 5'-most EST jC-gmro02910029a02d1

Seq. No. 27228
 Contig ID 152262_1.R1040
 5'-most EST g4397342

Seq. No. 27229
 Contig ID 152289_1.R1040
 5'-most EST pcp700991276.h1

Seq. No. 27230
 Contig ID 152306_1.R1040
 5'-most EST zhf700961049.h1
 Method BLASTX
 NCBI GI g3024426
 BLAST score 143

E value 5.0e-09
 Match length 90
 % identity 44
 NCBI Description PYRUVATE, PHOSPHATE DIKINASE PRECURSOR
 (PYRUVATE, ORTHOPHOSPHATE DIKINASE) >gi_1084302_pir_S55478
 pyruvate, orthophosphate dikinase (EC 2.7.9.1) - common ice
 plant >gi_854265_emb_CAA57872_ (X82489)
 pyruvate, orthophosphate dikinase [Mesembryanthemum
 crystallinum]

Seq. No. 27231
 Contig ID 152323_1.R1040
 5'-most EST leu701149479.h1
 Method BLASTX
 NCBI GI g4455299
 BLAST score 264
 E value 3.0e-23
 Match length 73
 % identity 75
 NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 27232
 Contig ID 152332_1.R1040
 5'-most EST epX701108066.h1

Seq. No. 27233
 Contig ID 152345_1.R1040
 5'-most EST zhF700954390.h1

Seq. No. 27234
 Contig ID 152397_1.R1040
 5'-most EST pcp700991432.h1
 Method BLASTX
 NCBI GI g2865433
 BLAST score 142
 E value 7.0e-09
 Match length 81
 % identity 37
 NCBI Description (AF039374) chromomethylase [Arabidopsis suecica]

Seq. No. 27235
 Contig ID 152399_1.R1040
 5'-most EST jC-gmle01810047e05a1
 Method BLASTX
 NCBI GI g541816
 BLAST score 1689
 E value 0.0e+00
 Match length 398
 % identity 81
 NCBI Description protein kinase - common ice plant >gi_457689_emb_CAA82990_
 (Z30329) protein kinase [Mesembryanthemum crystallinum]

Seq. No. 27236
 Contig ID 152410_1.R1040
 5'-most EST smc700746390.h1

Seq. No. 27237

Contig ID	152421_1.R1040
5'-most EST	rlr700896803.h1
Method	BLASTX
NCBI GI	g4309698
BLAST score	399
E value	1.0e-38
Match length	133
% identity	65
NCBI Description	(AC006266) putative glucosyltransferase [Arabidopsis thaliana]
Seq. No.	27238
Contig ID	152428_1.R1040
5'-most EST	dpv701102248.h1
Seq. No.	27239
Contig ID	152430_1.R1040
5'-most EST	pcp700991510.h1
Seq. No.	27240
Contig ID	152435_1.R1040
5'-most EST	eep700866705.h1
Method	BLASTX
NCBI GI	g3702332
BLAST score	141
E value	1.0e-15
Match length	85
% identity	45
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.	27241
Contig ID	152449_1.R1040
5'-most EST	pcp700991553.h1
Method	BLASTX
NCBI GI	g4220514
BLAST score	376
E value	4.0e-36
Match length	142
% identity	57
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]
Seq. No.	27242
Contig ID	152456_1.R1040
5'-most EST	pmv700892711.h1
Seq. No.	27243
Contig ID	152459_1.R1040
5'-most EST	pcp700991575.h1
Method	BLASTX
NCBI GI	g1854386
BLAST score	236
E value	5.0e-20
Match length	56
% identity	73
NCBI Description	(AB001375) similar to soluble NSF attachment protein [Vitis vinifera]

BLAST score	353
E value	3.0e-44
Match length	136
% identity	67
NCBI Description	(AC006569) putative serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	27250
Contig ID	152601_1.R1040
5'-most EST	pcp700991775.h1
Seq. No.	27251
Contig ID	152625_1.R1040
5'-most EST	jC-gmst02400053f11d1
Seq. No.	27252
Contig ID	152638_1.R1040
5'-most EST	jC-gmf102220064f05a1
Method	BLASTX
NCBI GI	g4508083
BLAST score	225
E value	2.0e-18
Match length	67
% identity	73
NCBI Description	(AC005882) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	27253
Contig ID	152645_1.R1040
5'-most EST	jC-gmro02910074g05d1
Seq. No.	27254
Contig ID	152659_1.R1040
5'-most EST	pcp700991863.h1
Method	BLASTX
NCBI GI	g1001263
BLAST score	497
E value	3.0e-51
Match length	177
% identity	59
NCBI Description	(D64003) hypothetical protein [Synechocystis sp.]
Seq. No.	27255
Contig ID	152686_1.R1040
5'-most EST	zhf700957194.h1
Method	BLASTX
NCBI GI	g4415931
BLAST score	564
E value	3.0e-58
Match length	137
% identity	76
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana] >gi_4559393_gb_AAD23053.1 AC006526_18 (AC006526) unknown protein [Arabidopsis thaliana]
Seq. No.	27256
Contig ID	152695_1.R1040
5'-most EST	pcp700991916.h1

Seq. No. 27269
 Contig ID 152908_1.R1040
 5'-most EST pcp700992291.h1

Seq. No. 27270
 Contig ID 152910_1.R1040
 5'-most EST pcp700992296.h1
 Method BLASTX
 NCBI GI g2826900
 BLAST score 446
 E value 2.0e-44
 Match length 135
 % identity 59
 NCBI Description (AB004461) DNA polymerase alpha catalytic subunit [Oryza sativa]

Seq. No. 27271
 Contig ID 152911_1.R1040
 5'-most EST jC-gmle01810084g05a1
 Method BLASTX
 NCBI GI g2245095
 BLAST score 209
 E value 1.0e-16
 Match length 66
 % identity 58
 NCBI Description (Z97343) formyltransferase purU homolog [Arabidopsis thaliana]

Seq. No. 27272
 Contig ID 152930_1.R1040
 5'-most EST pcp700992322.h1
 Method BLASTX
 NCBI GI g4490316
 BLAST score 595
 E value 1.0e-61
 Match length 156
 % identity 64
 NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No. 27273
 Contig ID 152979_1.R1040
 5'-most EST pcp700992394.h1

Seq. No. 27274
 Contig ID 152982_1.R1040
 5'-most EST uC-gmflminsoy077g08b1
 Method BLASTX
 NCBI GI g4567250
 BLAST score 275
 E value 3.0e-24
 Match length 83
 % identity 58
 NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No. 27275
 Contig ID 152987_1.R1040
 5'-most EST gsv701046566.h1

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Seq. No.	27316
Contig ID	153642_1.R1040
5'-most EST	rca700996494.h1

Seq. No.	27318
Contig ID	153653_1.R1040
5'-most EST	uC-qmrõminsoyl22b10b1

Seq. No.	27319
Contig ID	153695_1.R1040
5'-most EST	uC-qmröpic031f04b1

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Seq. No.          27320
Contig ID         153713_1.R1040
5'-most EST      pcp700995761.h1
Method            BLASTN
NCBI GI           g2564336
BLAST score       120
E value           6.0e-61
Match length      264
% identity        86
NCBI Description  Brassica campestris mRNA for Tat binding protein 1,
                  complete cds
```

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Contig ID 153861_1.R1040
5'-most EST pcp700993951.h1

Seq. No.	27328
Contig ID	153867_1.R1040
5'-most EST	zhf700958665.h1

Seq. No.	27329
Contig ID	153873_1.R1040
5'-most EST	pcp700993969.h1

Seq. No.	27330
Contig ID	153879_1.R1040
5'-most EST	pcp700993978.h1

Seq. No.	27331
Contig ID	153895_1.R1040
5'-most EST	pcp700994004.h1

Seq. No.	27332
Contig ID	153919_1.R1040
5'-most EST	uC-gmrōminsoy300g11b1

```
Seq. No.          27333
Contig ID         153935_1.R1040
5'-most EST      rca700999021.h1
Method            BLASTX
NCBI GI           g3924613
BLAST score       227
E value           5.0e-27
Match length      147
% identity        54
NCBI Description  (AF069442) hypothetical protein [Arabidopsis thaliana]
                  >gi_4263512_gb_AAD15338_ (AC004044) hypothetical protein
                  [Arabidopsis thaliana]
```

Seq. No.	27334
Contig ID	153935_2.R1040
5'-most EST	fC-gmr0700864959d3

Seq. No.	27335
Contig ID	153938_1.R1040
5'-most EST	pmv700888824.h1

Seq. No.	27336
Contig ID	153941_1.R1040
5'-most EST	uC-gmrominsoy304h12b1

Seq. No.	27337
Contig ID	153941_2.R1040
5'-most EST	jC-gmf102220113e06d1

Seq. No.	27338
Contig ID	153943_1.R1040
5'-most EST	uC-gmfl̄minsoy010d11b1

Seq. No. 27339

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Seq. No.          27353
Contig ID         154108_1.R1040
5'-most EST      fC-gmle7000741294a1
Method            BLASTX
NCBI GI           g3021270
BLAST score       687
E value           2.0e-72
Match length      191
% identity        69
NCBI Description  (AL022347) serine/threonine kinase -like protein
                  [Arabidopsis thaliana]
```

```
Seq. No.          27355
Contig ID         154143_1.R1040
5'-most EST      uC-gmröminsoyl25f07b1
Method            BLASTX
NCBI GI           g2160694
BLAST score       927
E value           1.0e-100
Match length      231
% identity         74
NCBI Description  (U73528) B' regulatory subunit of PP2A [Arabidopsis
                  thaliana]
```

```
Seq. No.          27357
Contig ID         154165_1.R1040
5'-most EST      pcp700994404.h1
Method           BLASTX
NCBI GI          g3183077
BLAST score       227
E value          4.0e-28
Match length      156
% identity        48
NCBI Description  PROBABLE 1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE
                  (DHNA-OCTAPRENYLTRANSFERASE) >gi_1653114_dbj_BAA18030_
                  (D90911) menaquinone biosynthesis protein [Synechocystis
```


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Seq. No.          27359
Contig ID         154239_1.R1040
5'-most EST      leu701152401.h1
Method            BLASTX
NCBI GI           g1076580
BLAST score       242
E value           1.0e-20
Match length      72
% identity        61
NCBI Description  alcohol dehydrogenase homolog ADH3b - tomato
                  >gi_913446_bbs_160508 (S75487) alcohol dehydrogenase ADH
                  {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red
                  cherry, Peptide, 390 aa] [Lycopersicon esculentum]
```

```
Seq. No.      27360
Contig ID     154260_1.R1040
5'-most EST   pmv700893490.h1
Method        BLASTX
NCBI GI       g3947613
BLAST score    205
E value       2.0e-16
Match length   82
% identity     46
NCBI Description (AL023828) cDNA EST EMBL:M89008 comes from this gene; cDNA
EST yk282d3.5 comes from this gene [Caenorhabditis elegans]
```

```
Seq. No..      27361
Contig ID      154271_1.R1040
5'-most EST    pcp700994568.h2
```

```
Seq. No.          27362
Contig ID         154327_1.R1040
5'-most EST      fua701037573.h1
Method           BLASTX
NCBI GI          g3688173
BLAST score       461
E value          4.0e-46
Match length      121
% identity        65
NCBI Description  (AL031804) putative protein [Arabidopsis thaliana]
```

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5'-most EST gsv701045552.h1
 Method BLASTX
 NCBI GI g2245115
 BLAST score 208
 E value 2.0e-16
 Match length 126
 % identity 39
 NCBI Description (297343) unnamed protein product [Arabidopsis thaliana]

Seq. No. 27401
 Contig ID 154732_1.R1040
 5'-most EST pcp700995353.h1

Seq. No. 27402
 Contig ID 154732_2.R1040
 5'-most EST asn701135077.h1

Seq. No. 27403
 Contig ID 154736_1.R1040
 5'-most EST pcp700995357.h1

Seq. No. 27404
 Contig ID 154754_1.R1040
 5'-most EST epX701108951.h1
 Method BLASTX
 NCBI GI g3327389
 BLAST score 665
 E value 5.0e-70
 Match length 145
 % identity 81
 NCBI Description (AC004483) putative DNA replication licensing factor, mcm5 [Arabidopsis thaliana]

Seq. No. 27405
 Contig ID 154770_1.R1040
 5'-most EST uC-gmronoir019f07b1
 Method BLASTX
 NCBI GI g421980
 BLAST score 363
 E value 1.0e-34
 Match length 87
 % identity 76
 NCBI Description transforming protein (myb3) - barley
 >gi_19059_emb_CAA50223_ (X70878) MybHv33 [Hordeum vulgare]

Seq. No. 27406
 Contig ID 154789_1.R1040
 5'-most EST pcp700995433.h1

Seq. No. 27407
 Contig ID 154801_1.R1040
 5'-most EST uC-gmflminsoy118d08b1
 Method BLASTX
 NCBI GI g4530126
 BLAST score 413
 E value 2.0e-43
 Match length 157

Seq. No. 27437
 Contig ID 155167_1.R1040
 5'-most EST kl1701213878.h1

Seq. No. 27438
 Contig ID 155174_1.R1040
 5'-most EST kmv700737763.h1

Seq. No. 27439
 Contig ID 155198_1.R1040
 5'-most EST kmv700737793.h1
 Method BLASTX
 NCBI GI g3047111
 BLAST score 271
 E value 5.0e-35
 Match length 171
 % identity 52
 NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 27440
 Contig ID 155214_1.R1040
 5'-most EST kmv700737815.h1

Seq. No. 27441
 Contig ID 155218_1.R1040
 5'-most EST zpv700762681.h1

Seq. No. 27442
 Contig ID 155247_1.R1040
 5'-most EST kmv700737967.h1
 Method BLASTX
 NCBI GI g3184061
 BLAST score 143
 E value 3.0e-09
 Match length 77
 % identity 42
 NCBI Description (AL023776) atp dependent helicase [Schizosaccharomyces pombe]

Seq. No. 27443
 Contig ID 155267_1.R1040
 5'-most EST sat701009238.h1
 Method BLASTX
 NCBI GI g4388717
 BLAST score 821
 E value 4.0e-88
 Match length 199
 % identity 78
 NCBI Description (AC006413) putative nuclear phosphoprotein (contains multiple TPR repeats prosite:QDOC50005) [Arabidopsis thaliana]

Seq. No. 27444
 Contig ID 155284_1.R1040
 5'-most EST jsh701068504.h1

Seq. No. 27445

E value 4.0e-85
 Match length 377
 % identity 86
 NCBI Description Pisum sativum aspartate carbamoyltransferase (pyrB1) mRNA, complete cds

Seq. No. 27515
 Contig ID 156448_1.R1040
 5'-most EST jC-gmf102220077f06d1
 Method BLASTX
 NCBI GI g2804280
 BLAST score 198
 E value 3.0e-15
 Match length 63
 % identity 57
 NCBI Description (AB003687) 6-4 photolyase [Arabidopsis thaliana]
 >gi_3929918_dbj_BAA34711_ (AB017331) 6-4 photolyase
 [Arabidopsis thaliana]

Seq. No. 27516
 Contig ID 156458_1.R1040
 5'-most EST kmv700739866.h1

Seq. No. 27517
 Contig ID 156473_1.R1040
 5'-most EST eep700867371.h1
 Method BLASTX
 NCBI GI g4455363
 BLAST score 313
 E value 2.0e-28
 Match length 142
 % identity 40
 NCBI Description (AL035524) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No. 27518
 Contig ID 156506_1.R1040
 5'-most EST g5666770
 Method BLASTX
 NCBI GI g4490316
 BLAST score 212
 E value 5.0e-17
 Match length 96
 % identity 55
 NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No. 27519
 Contig ID 156520_1.R1040
 5'-most EST fC-gmle700739977a1
 Method BLASTX
 NCBI GI g2997593
 BLAST score 259
 E value 9.0e-23
 Match length 89
 % identity 57
 NCBI Description (AF020816) glucose-6-phosphate/phosphate-translocator precursor [Solanum tuberosum]

[illegible]

06-987

[illegible][illegible][illegible][illegible][illegible][illegible]

08-06-10

06-08-1973

06-08-1973

thaliana]

Seq. No. 27555
 Contig ID 157220_1.R1040
 5'-most EST hrw701061188.h1

Seq. No. 27556
 Contig ID 157221_1.R1040
 5'-most EST rca700997763.h1
 Method BLASTX
 NCBI GI g3319713
 BLAST score 1046
 E value 1.0e-114
 Match length 272
 % identity 71
 NCBI Description (AJ006992) chitinase precursor [Canavalia ensiformis]

Seq. No. 27557
 Contig ID 157237_1.R1040
 5'-most EST kmv700741105.h1

Seq. No. 27558
 Contig ID 157244_1.R1040
 5'-most EST kmv700741112.h1

Seq. No. 27559
 Contig ID 157324_1.R1040
 5'-most EST uC-gmflminsoy099b09b1

Seq. No. 27560
 Contig ID 157332_1.R1040
 5'-most EST bnu700967559.h1

Seq. No. 27561
 Contig ID 157336_1.R1040
 5'-most EST smc700747435.h1
 Method BLASTX
 NCBI GI g2501296
 BLAST score 217
 E value 6.0e-18
 Match length 87
 % identity 49
 NCBI Description DNA GYRASE SUBUNIT B >gi_1652801_dbj_BAA17720_ (D90908) DNA gyrase B subunit [Synechocystis sp.]

Seq. No. 27562
 Contig ID 157345_1.R1040
 5'-most EST kmv700741250.h1
 Method BLASTX
 NCBI GI g3493253
 BLAST score 159
 E value 3.0e-11
 Match length 64
 % identity 50
 NCBI Description (AF076156) catechol-O-methyltransferase [Mus musculus]

Seq. No. 27563

Seq. No. 27580
 Contig ID 157712_1.R1040
 5'-most EST jC-gmst02400049h05d1

Seq. No. 27581
 Contig ID 157713_1.R1040
 5'-most EST kmv700743793.h1
 Method BLASTX
 NCBI GI g3775987
 BLAST score 173
 E value 7.0e-13
 Match length 51
 % identity 65
 NCBI Description (AJ010457) RNA helicase [Arabidopsis thaliana]

Seq. No. 27582
 Contig ID 157728_1.R1040
 5'-most EST kmv700741821.h1
 Method BLASTN
 NCBI GI g4519184
 BLAST score 53
 E value 4.0e-21
 Match length 117
 % identity 86
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15F13, complete sequence

Seq. No. 27583
 Contig ID 157739_1.R1040
 5'-most EST xzm700763715.h1

Seq. No. 27584
 Contig ID 157754_2.R1040
 5'-most EST cle700967748.h1
 Method BLASTX
 NCBI GI g3063455
 BLAST score 313
 E value 6.0e-29
 Match length 72
 % identity 76
 NCBI Description (AC003981) F22013.17 [Arabidopsis thaliana]

Seq. No. 27585
 Contig ID 157782_1.R1040
 5'-most EST smc700748556.h1

Seq. No. 27586
 Contig ID 157783_1.R1040
 5'-most EST jC-gmro02910038f02a1
 Method BLASTX
 NCBI GI g3080401
 BLAST score 337
 E value 1.0e-31
 Match length 95
 % identity 67
 NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

>gi_4455265_emb_CAB36801.1_ (AL035527) putative protein
[Arabidopsis thaliana]

Seq. No. 27587
Contig ID 157801_1.R1040
5'-most EST kmv700741935.h1

Seq. No. 27588
Contig ID 157830_1.R1040
5'-most EST jC-gmro02800031e05a1

Seq. No. 27589
Contig ID 157843_1.R1040
5'-most EST kmv700742008.h1

Seq. No. 27590
Contig ID 157865_1.R1040
5'-most EST kmv700742049.h1
Method BLASTN
NCBI GI g510545
BLAST score 157
E value 6.0e-83
Match length 285
% identity 89
NCBI Description P.sativum mRNA for starch branching enzyme I

Seq. No. 27591
Contig ID 157870_1.R1040
5'-most EST smc700747937.h1
Method BLASTX
NCBI GI g2388561
BLAST score 543
E value 1.0e-55
Match length 165
% identity 66
NCBI Description (AC000098) Similar to Arabidopsis hypothetical protein
PID:e326839 (gb_Z97337). [Arabidopsis thaliana]

Seq. No. 27592
Contig ID 157913_1.R1040
5'-most EST kmv700742131.h1

Seq. No. 27593
Contig ID 157920_1.R1040
5'-most EST kmv700742139.h1
Method BLASTX
NCBI GI g1168235
BLAST score 185
E value 2.0e-14
Match length 41
% identity 88
NCBI Description 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING
>gi_1073800_pir_C64077 6-phosphogluconate dehydrogenase,
decarboxylating (gnd) homolog - Haemophilus influenzae
(strain Rd KW20) >gi_1573539 (U32737) 6-phosphogluconate
dehydrogenase, decarboxylating (gnd) [Haemophilus
influenzae Rd]

Match length	138
% identity	62
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]
Seq. No.	27625
Contig ID	158768_1.R1040
5'-most EST	zhf700960112.h1
Seq. No.	27626
Contig ID	158804_1.R1040
5'-most EST	kmv700743942.h1
Method	BLASTX
NCBI GI	g1903360
BLAST score	188
E value	4.0e-14
Match length	123
% identity	37
NCBI Description	(AC000104) Similar to Arabidopsis 2A6 (gb_X83096). EST gb_T76913 comes from this gene. [Arabidopsis thaliana]
Seq. No.	27627
Contig ID	158842_1.R1040
5'-most EST	kmv700744008.h1
Seq. No.	27628
Contig ID	158954_1.R1040
5'-most EST	rca700996387.h1
Seq. No.	27629
Contig ID	158989_1.R1040
5'-most EST	uC-gmrönoir057f06b1
Seq. No.	27630
Contig ID	158994_1.R1040
5'-most EST	leu701148728.h1
Seq. No.	27631
Contig ID	158997_1.R1040
5'-most EST	smw700646229.h1
Seq. No.	27632
Contig ID	159036_1.R1040
5'-most EST	ary700764309.h1
Method	BLASTX
NCBI GI	g3377803
BLAST score	601
E value	2.0e-62
Match length	200
% identity	61
NCBI Description	(AF075597) Similar to (p)ppGpp synthetase; T2H3.9 [Arabidopsis thaliana]
Seq. No.	27633
Contig ID	159055_1.R1040
5'-most EST	smc700744206.h1
Method	BLASTX
NCBI GI	g4263704

Method	BLASTX
NCBI GI	g4455359
BLAST score	348
E value	4.0e-33
Match length	106
% identity	64
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]
Seq. No.	27643
Contig ID	159317_1.R1040
5'-most EST	smc700744707.h1
Method	BLASTX
NCBI GI	g2244763
BLAST score	339
E value	4.0e-37
Match length	104
% identity	72
NCBI Description	(Z97335) A6 anther-specific protein [Arabidopsis thaliana]
Seq. No.	27644
Contig ID	159354_1.R1040
5'-most EST	uC-gmrominsoy050a03b1
Method	BLASTX
NCBI GI	g2827699
BLAST score	150
E value	2.0e-09
Match length	84
% identity	40
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.	27645
Contig ID	159363_1.R1040
5'-most EST	jC-gmst02400027c08a1
Method	BLASTX
NCBI GI	g4467111
BLAST score	518
E value	2.0e-60
Match length	163
% identity	67
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]
Seq. No.	27646
Contig ID	159414_1.R1040
5'-most EST	hrw701061205.h1
Seq. No.	27647
Contig ID	159468_1.R1040
5'-most EST	smc700745014.h1
Method	BLASTX
NCBI GI	g4433381
BLAST score	211
E value	3.0e-17
Match length	75
% identity	57
NCBI Description	(D50034) 4-coumarate:CoA ligase [Nicotiana tabacum]
Seq. No.	27648

Method	BLASTX
NCBI GI	g3172025
BLAST score	210
E value	6.0e-17
Match length	70
% identity	66
NCBI Description	(AB005805) aldehyde oxidase [Arabidopsis thaliana]
Seq. No.	27671
Contig ID	159993_1.R1040
5'-most EST	zhf700951771.h1
Seq. No.	27672
Contig ID	160011_1.R1040
5'-most EST	kl1701206372.h1
Method	BLASTX
NCBI GI	g3355464
BLAST score	246
E value	5.0e-21
Match length	118
% identity	47
NCBI Description	(AC004218) putative ATP-binding-cassette protein, 3' partial [Arabidopsis thaliana]
Seq. No.	27673
Contig ID	160016_1.R1040
5'-most EST	smc700746184.h1
Seq. No.	27674
Contig ID	160042_1.R1040
5'-most EST	smc700746222.h1
Seq. No.	27675
Contig ID	160049_1.R1040
5'-most EST	smc700746233.h1
Seq. No.	27676
Contig ID	160064_1.R1040
5'-most EST	smc700746265.h1
Seq. No.	27677
Contig ID	160071_1.R1040
5'-most EST	g5753341
Method	BLASTX
NCBI GI	g2288982
BLAST score	357
E value	8.0e-34
Match length	111
% identity	68
NCBI Description	(AC002335) hypothetical protein [Arabidopsis thaliana]
Seq. No.	27678
Contig ID	160071_2.R1040
5'-most EST	jex700908256.h1
Seq. No.	27679
Contig ID	160087_1.R1040

NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 27685
Contig ID 160107_1.R1040
5'-most EST zzp700833586.h1

Seq. No. 27686
Contig ID 160111_1.R1040
5'-most EST jC-gmro02800035c06a1
Method BLASTX
NCBI GI g4467125
BLAST score 604
E value 3.0e-81
Match length 200
% identity 73

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 27687
Contig ID 160129_1.R1040
5'-most EST pmv700889726.h1
Method BLASTX
NCBI GI g4426611
BLAST score 156
E value 2.0e-10
Match length 106
% identity 32

NCBI Description (AF096897) pushover [Drosophila melanogaster]

Seq. No. 27688
Contig ID 160141_1.R1040
5'-most EST smc700746360.h1

Seq. No. 27689
Contig ID 160148_1.R1040
5'-most EST smc700746369.h1

Seq. No. 27690
Contig ID 160156_1.R1040
5'-most EST dpv701099069.h1
Method BLASTN
NCBI GI g218261
BLAST score 92
E value 2.0e-44
Match length 180
% identity 88

NCBI Description Soybean mRNA for early nodulin

Seq. No. 27691
Contig ID 160163_1.R1040
5'-most EST zpv700759810.h1
Method BLASTX
NCBI GI g3193310
BLAST score 356
E value 1.0e-33
Match length 130
% identity 52

NCBI Description (AF069300) contains similarity to Nicotiana tabacum hin1

[illegible]

Seq. No.	27720
Contig ID	160703_1.R1040
5'-most EST	smc700747185.h1

Seq. No.	27722
Contig ID	160712_1.R1040
5'-most EST	awf700840345.h1

Seq. No.	27724
Contig ID	160746_1.R1040
5'-most EST	smc700747234.h1

Seq. No.	27725
Contig ID	160765_1.R1040
5'-most EST	smc700747259.h1

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Seq. No.          27726
Contig ID         160808_1.R1040
5'-most EST      uC-gmröpic045e04b1
Method            BLASTX
NCBI GI           g4490319
BLAST score       161
E value           1.0e-10
Match length      141
% identity        33
NCBI Description  (AL035678) metal-transporting P-type ATPase [Arabidopsis
                  thaliana]
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4306

Seq. No.	27737
Contig ID	160983_1.R1040
5'-most EST	smc700747596.h1
Method	BLASTX
NCBI GI	g1752734
BLAST score	218
E value	5.0e-18
Match length	85
% identity	49
NCBI Description	(D78510) beta-glucan-elicitor receptor [Glycine max]
Seq. No.	27738
Contig ID	160985_1.R1040
5'-most EST	uC-gmrominsoy320g06b1
Seq. No.	27739
Contig ID	160992_1.R1040
5'-most EST	smc700747620.h1
Seq. No.	27740
Contig ID	161005_1.R1040
5'-most EST	fde700871538.h1
Seq. No.	27741
Contig ID	161006_1.R1040
5'-most EST	jC-gmro02910007d03d1
Seq. No.	27742
Contig ID	161056_1.R1040
5'-most EST	uC-gmropic008f11b1
Method	BLASTX
NCBI GI	g2088651
BLAST score	349
E value	6.0e-33
Match length	121
% identity	55
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]
Seq. No.	27743
Contig ID	161065_1.R1040
5'-most EST	zsg701128088.h1
Method	BLASTX
NCBI GI	g3550588
BLAST score	277
E value	2.0e-24
Match length	143
% identity	49
NCBI Description	(AJ010643) heat shock transcription factor (HSFA) [Pisum sativum]
Seq. No.	27744
Contig ID	161165_1.R1040
5'-most EST	k11701210268.h1
Method	BLASTX
NCBI GI	q3135265

BLAST score 216
 E value 6.0e-24
 Match length 114
 % identity 50
 NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]

Seq. No. 27745
 Contig ID 161172_1.R1040
 5'-most EST rca700998634.h1

Seq. No. 27746
 Contig ID 161183_1.R1040
 5'-most EST zhf700957607.h1

Seq. No. 27747
 Contig ID 161199_1.R1040
 5'-most EST smc700747996.h1
 Method BLASTX
 NCBI GI g4140691
 BLAST score 174
 E value 8.0e-13
 Match length 69
 % identity 55
 NCBI Description (AF101972) zeatin O-glucosyltransferase [Phaseolus lunatus]

Seq. No. 27748
 Contig ID 161214_1.R1040
 5'-most EST uC-gmropic102g11b1
 Method BLASTX
 NCBI GI g2129953
 BLAST score 505
 E value 3.0e-51
 Match length 127
 % identity 69
 NCBI Description laccase (EC 1.10.3.2) - common tobacco >gi_1685087 (U43542),
 diphenol oxidase [Nicotiana tabacum]

Seq. No. 27749
 Contig ID 161276_1.R1040
 5'-most EST rca700997496.h1

Seq. No. 27750
 Contig ID 161302_1.R1040
 5'-most EST rca700998578.h1
 Method BLASTX
 NCBI GI g3319345
 BLAST score 143
 E value 3.0e-09
 Match length 86
 % identity 33
 NCBI Description (AF077407) contains similarity to maize transposon MuDR
 (GB:M76978) [Arabidopsis thaliana]

Seq. No. 27751
 Contig ID 161313_1.R1040
 5'-most EST zsg701126738.h1
 Method BLASTX

E value	2.0e-25
Match length	68
% identity	75
NCBI Description	(U50201) prunasin hydrolase precursor [Prunus serotina]
Seq. No.	27766
Contig ID	161531_2.R1040
5'-most EST	smc700748435.h1
Seq. No.	27767
Contig ID	161545_1.R1040
5'-most EST	asn701139424.h1
Method	BLASTX
NCBI GI	g2829887
BLAST score	306
E value	3.0e-28
Match length	93
% identity	70
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	27768
Contig ID	161550_1.R1040
5'-most EST	fC-gmro7000748459f1
Method	BLASTX
NCBI GI	g2760839
BLAST score	260
E value	2.0e-22
Match length	169
% identity	25
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]
Seq. No.	27769
Contig ID	161570_1.R1040
5'-most EST	uC-gmronoir052g11b1
Method	BLASTX
NCBI GI	g3367578
BLAST score	464
E value	3.0e-46
Match length	120
% identity	69
NCBI Description	(AL031135) protein kinase - like protein [Arabidopsis thaliana]
Seq. No.	27770
Contig ID	161576_1.R1040
5'-most EST	uC-gmrominsoy312h07b1
Method	BLASTN
NCBI GI	g3643588
BLAST score	52
E value	5.0e-20
Match length	116
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	27771
Contig ID	161577_1.R1040

5'-most EST	zhf700952184.h1
Method	BLASTX
NCBI GI	g4455307
BLAST score	542
E value	2.0e-55
Match length	106
% identity	91
NCBI Description	(AL035528) methionyl-tRNA synthetase-like protein [Arabidopsis thaliana]
Seq. No.	27772
Contig ID	161604 1.R1040
5'-most EST	fC-gmro700748540a2
Method	BLASTX
NCBI GI	g4539320
BLAST score	562
E value	6.0e-58
Match length	152
% identity	63
NCBI Description	(AL035679) putative endo-1, 4-beta-glucanase [Arabidopsis thaliana]
Seq. No.	27773
Contig ID	161607 1.R1040
5'-most EST	smc700748580.h1
Seq. No.	27774
Contig ID	161610 1.R1040
5'-most EST	smc700748551.h1
Seq. No.	27775
Contig ID	161650 1.R1040
5'-most EST	smc700748596.h1
Seq. No.	27776
Contig ID	161667 1.R1040
5'-most EST	smc700748623.h1
Seq. No.	27777
Contig ID	161727 1.R1040
5'-most EST	bth700847982.h1
Method	BLASTX
NCBI GI	g112947
BLAST score	202
E value	8.0e-16
Match length	88
% identity	31
NCBI Description	AAC-RICH MRNA CLONE AAC3 PROTEIN >gi_84121_pir_S05357 hypothetical protein (clone AAC3) - slime mold (Dictyostelium discoideum) (fragment) >gi_7176_emb_CAA34531 (X16524) coding region (AA 1 - 437) [Dictyostelium discoideum]
Seq. No.	27778
Contig ID	161758 1.R1040
5'-most EST	smc700748749.h1

5'-most EST smc700748888.h1
 Method BLASTX
 NCBI GI g3786009
 BLAST score 379
 E value 7.0e-37
 Match length 87
 % identity 82
 NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 27786
 Contig ID 161865_1.R1040
 5'-most EST gsv701047952.h1

Seq. No. 27787
 Contig ID 161881_1.R1040
 5'-most EST fC-gmro7000748929a1
 Method BLASTX
 NCBI GI g2760836
 BLAST score 202
 E value 2.0e-15
 Match length 111
 % identity 40
 NCBI Description (AC003105) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No. 27788
 Contig ID 161885_1.R1040
 5'-most EST zlv700807563.h1

Seq. No. 27789
 Contig ID 161912_1.R1040
 5'-most EST smc700749012.h1

Seq. No. 27790
 Contig ID 161913_1.R1040
 5'-most EST smc700749013.h1

Seq. No. 27791
 Contig ID 161922_1.R1040
 5'-most EST smc700749027.h1
 Method BLASTX
 NCBI GI g995714
 BLAST score 231
 E value 3.0e-23
 Match length 129
 % identity 44
 NCBI Description (X91258) L3177 [Saccharomyces cerevisiae]

Seq. No. 27792
 Contig ID 162005_1.R1040
 5'-most EST jsh701066291.h1

Seq. No. 27793
 Contig ID 162025_1.R1040
 5'-most EST smc700749221.h1
 Method BLASTX
 NCBI GI g4249402

mRNA, and translated products

Seq. No.	27808
Contig ID	162360_1.R1040
5'-most EST	smc700749822.h1
Method	BLASTX
NCBI GI	g3172025
BLAST score	559
E value	1.0e-57
Match length	140
% identity	75
NCBI Description	(AB005805) aldehyde oxidase [Arabidopsis thaliana]
Seq. No.	27809
Contig ID	162361_1.R1040
5'-most EST	uC-gmronoir049h07b1
Seq. No.	27810
Contig ID	162414_1.R1040
5'-most EST	uC-gmropic019e08b1
Seq. No.	27811
Contig ID	162419_1.R1040
5'-most EST	pmv700893728.h1
Method	BLASTX
NCBI GI	g4510377
BLAST score	146
E value	2.0e-09
Match length	76
% identity	36
NCBI Description	(AC007017) putative RNA helicase A [Arabidopsis thaliana]
Seq. No.	27812
Contig ID	162420_1.R1040
5'-most EST	dpr701101092.h1
Seq. No.	27813
Contig ID	162447_1.R1040
5'-most EST	smc700749945.h1
Seq. No.	27814
Contig ID	162452_1.R1040
5'-most EST	smc700749951.h1
Method	BLASTX
NCBI GI	g3413700
BLAST score	388
E value	1.0e-37
Match length	118
% identity	63
NCBI Description	(AC004747) putative YME1 protein [Arabidopsis thaliana]
Seq. No.	27815
Contig ID	162457_1.R1040
5'-most EST	smc700749958.h1
Seq. No.	27816
Contig ID	162466_1.R1040

5'-most EST smc700749970.h1

Seq. No. 27817
Contig ID 162487_1.R1040
5'-most EST smc700750012.h1

Seq. No. 27818
Contig ID 162502_1.R1040
5'-most EST fC-gmro700750041a2
Method BLASTX
NCBI GI g4138209
BLAST score 309
E value 3.0e-28
Match length 140
% identity 43
NCBI Description (AJ223071) serine/threonine kinase protein MSTK2L, long-form [Mus musculus]

Seq. No. 27819
Contig ID 162513_1.R1040
5'-most EST uC-gmropic108f03b1
Method BLASTX
NCBI GI g1946367
BLAST score 330
E value 3.0e-30
Match length 176
% identity 39
NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 27820
Contig ID 162513_2.R1040
5'-most EST uC-gmropic037c12b1
Method BLASTX
NCBI GI g3738298
BLAST score 157
E value 9.0e-16
Match length 77
% identity 56
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
>gi_4249394 (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 27821
Contig ID 162514_1.R1040
5'-most EST uC-gmrominsoyl28d07b1

Seq. No. 27822
Contig ID 162530_1.R1040
5'-most EST uC-gmropic106c05b1

Seq. No. 27823
Contig ID 162532_1.R1040
5'-most EST kl1701214995.h1
Method BLASTX
NCBI GI g3063451
BLAST score 182
E value 3.0e-28

Match length	143
% identity	51
NCBI Description	(AC003981) F22013.13 [Arabidopsis thaliana]
Seq. No.	27824
Contig ID	162540_1.R1040
5'-most EST	uC-gmflminsoy065h02b1
Seq. No.	27825
Contig ID	162543_1.R1040
5'-most EST	uC-gmrominsoy138e10b1
Seq. No.	27826
Contig ID	162562_1.R1040
5'-most EST	fC-gmro700750148a2
Method	BLASTX
NCBI GI	g2935300
BLAST score	602
E value	1.0e-62
Match length	135
% identity	84
NCBI Description	(AF038046) 3-hydroxy-3-methylglutaryl-coenzyme A reductase 2 [Gossypium hirsutum]
Seq. No.	27827
Contig ID	162574_1.R1040
5'-most EST	rca700998968.h1
Seq. No.	27828
Contig ID	162582_1.R1040
5'-most EST	crh700851350.h1
Seq. No.	27829
Contig ID	162624_1.R1040
5'-most EST	smc700750249.h1
Seq. No.	27830
Contig ID	162632_1.R1040
5'-most EST	sat701009548.h1
Seq. No.	27831
Contig ID	162649_1.R1040
5'-most EST	fC-gmro700750285a2
Method	BLASTX
NCBI GI	g1888357
BLAST score	624
E value	7.0e-65
Match length	227
% identity	57
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_(Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]
Seq. No.	27832
Contig ID	162661_1.R1040
5'-most EST	kl1701212328.h1

BLAST score 249
 E value 4.0e-21
 Match length 165
 % identity 35
 NCBI Description SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68)
 >gi_108065_pir_S12981 68K protein - gray wolf
 >gi_227342_prf_1702226A SRP68 protein [Canis familiaris]

Seq. No. 27850
 Contig ID 162964_1.R1040
 5'-most EST hrw701062474.h1

Seq. No. 27851
 Contig ID 162965_1.R1040
 5'-most EST pxt700945737.h1

Seq. No. 27852
 Contig ID 162980_1.R1040
 5'-most EST jsh701068517.h1

Seq. No. 27853
 Contig ID 162987_1.R1040
 5'-most EST zhf700963936.h1

Seq. No. 27854
 Contig ID 162991_1.R1040
 5'-most EST uC-gmropic021g10b1
 Method BLASTX
 NCBI GI g1419036
 BLAST score 438
 E value 2.0e-43
 Match length 116
 % identity 78
 NCBI Description (X98421) delta-1-pyrroline-5-carboxylate synthase [Medicago sativa]

Seq. No. 27855
 Contig ID 162991_2.R1040
 5'-most EST jC-gmro02910066g03a1
 Method BLASTX
 NCBI GI g1709534
 BLAST score 460
 E value 4.0e-46
 Match length 140
 % identity 69
 NCBI Description DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE A (P5CS A)
 [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK);
 GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR)
 (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE)
 (GLUTAMYL-GAMMA-SEMIALDE... >gi_2129572_pir_S66637
 delta-1-pyrroline-5-carboxylate synthetase - Arabidopsis
 thaliana >gi_829100_emb_CAA60740_ (X87330)
 pyrroline-5-carboxylate synthetase [Arabidopsis thaliana]
 >gi_870866_emb_CAA60446_ (X86777) pyrroline-5-carboxylate
 synthetase A [Arabidopsis thaliana]
 >gi_1041248_emb_CAA61593_ (X89414) pyrroline-5-carboxylate
 synthase [Arabidopsis thaliana] >gi_2642162 (AC003000)

delta-1-pyrroline 5-carboxylase synthetase, P5C1
[Arabidopsis thaliana]

Seq. No. 27856
Contig ID 163015_1.R1040
5'-most EST ujr700646622.h1

Seq. No. 27857
Contig ID 163018_1.R1040
5'-most EST uC-gmrominsoy155b12b1

Seq. No. 27858
Contig ID 163055_1.R1040
5'-most EST ujr700646676.h1

Seq. No. 27859
Contig ID 163069_1.R1040
5'-most EST bth700844272.h1

Seq. No. 27860
Contig ID 163071_1.R1040
5'-most EST jC-gmro02910062c04a1

Seq. No. 27861
Contig ID 163080_1.R1040
5'-most EST vzy700750670.h1
Method BLASTN
NCBI GI g1947070
BLAST score 229
E value 1.0e-126
Match length 245
% identity 98
NCBI Description Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds

Seq. No. 27862
Contig ID 163094_1.R1040
5'-most EST g5057812
Method BLASTX
NCBI GI g3643082
BLAST score 348
E value 2.0e-32
Match length 100
% identity 64
NCBI Description (AF075579) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No. 27863
Contig ID 163101_1.R1040
5'-most EST vzy700750543.h1
Method BLASTX
NCBI GI g282881
BLAST score 237
E value 3.0e-20
Match length 82
% identity 56
NCBI Description receptor-like protein kinase precursor - Arabidopsis

0534016 101000

Match length 52
 % identity 46
 NCBI Description (AF017144) (1-4)-beta-mannan endohydrolase [*Lycopersicon
 esculentum*]

Seq. No. 27898
 Contig ID 163558_1.R1040
 5'-most EST pmv700894549.h1

Seq. No. 27899
 Contig ID 163567_1.R1040
 5'-most EST bth700846161.h1

Seq. No. 27900
 Contig ID 163587_1.R1040
 5'-most EST awf700843147.h1

Seq. No. 27901
 Contig ID 163609_1.R1040
 5'-most EST pmv700888988.h1

Seq. No. 27902
 Contig ID 163626_1.R1040
 5'-most EST vzy700751413.h1
 Method BLASTX
 NCBI GI g3281850
 BLAST score 555
 E value 3.0e-57
 Match length 125
 % identity 81
 NCBI Description (AL031004) monogalactosyldiacylglycerol synthase - like
 protein [*Arabidopsis thaliana*]

Seq. No. 27903
 Contig ID 163633_1.R1040
 5'-most EST vzy700751420.h1

Seq. No. 27904
 Contig ID 163645_1.R1040
 5'-most EST vzy700751441.h1

Seq. No. 27905
 Contig ID 163695_1.R1040
 5'-most EST vzy700751535.h1

Seq. No. 27906
 Contig ID 163712_1.R1040
 5'-most EST vzy700751804.h1
 Method BLASTX
 NCBI GI g32709
 BLAST score 288
 E value 3.0e-26
 Match length 81
 % identity 64
 NCBI Description (X62570) IFP53 [*Homo sapiens*]

Seq. No. 27907

5'-most EST zpv700763092.h1
 Method BLASTX
 NCBI GI g2492792
 BLAST score 294
 E value 2.0e-26
 Match length 93
 % identity 68
 NCBI Description LATE NODULIN 56 (N-56) >gi_532290_dbj_BAA07212_ (D38015)
 soybean late nodulin [Glycine max]

Seq. No. 27927
 Contig ID 164154_1.R1040
 5'-most EST epx701105636.h1

Seq. No. 27928
 Contig ID 164156_1.R1040
 5'-most EST vzy700752270.h1
 Method BLASTX
 NCBI GI g2668492
 BLAST score 198
 E value 3.0e-15
 Match length 151
 % identity 36
 NCBI Description (D89981) metal-transporting P-type ATPase [Arabidopsis
 thaliana]

Seq. No. 27929
 Contig ID 164175_1.R1040
 5'-most EST uC-gmropic035g09b1

Seq. No. 27930
 Contig ID 164205_1.R1040
 5'-most EST zhf700953905.h1

Seq. No. 27931
 Contig ID 164230_1.R1040
 5'-most EST epx701105604.h1

Seq. No. 27932
 Contig ID 164235_1.R1040
 5'-most EST uC-gmrominsoy215c09b1

Seq. No. 27933
 Contig ID 164269_1.R1040
 5'-most EST jex700907685.h1
 Method BLASTX
 NCBI GI g3342798
 BLAST score 305
 E value 8.0e-28
 Match length 105
 % identity 58
 NCBI Description (AF061240) glutamine cyclotransferase precursor [Carica
 papaya]

Seq. No. 27934
 Contig ID 164269_2.R1040
 5'-most EST fua701036923.h1

Method	BLASTX
NCBI GI	g3342798
BLAST score	199
E value	1.0e-15
Match length	49
% identity	78
NCBI Description	(AF061240) glutamine cyclotransferase precursor [Carica papaya]
Seq. No.	27935
Contig ID	164270_1.R1040
5'-most EST	pmv700893975.h1
Method	BLASTX
NCBI GI	g4220512
BLAST score	1125
E value	1.0e-123
Match length	258
% identity	79
NCBI Description	(AL035356) putative pectate lyase [Arabidopsis thaliana]
Seq. No.	27936
Contig ID	164277_1.R1040
5'-most EST	uC-gmrominsoyl02h05b1
Seq. No.	27937
Contig ID	164278_1.R1040
5'-most EST	vzy700752453.h1
Method	BLASTX
NCBI GI	g3046815
BLAST score	214
E value	5.0e-18
Match length	130
% identity	41
NCBI Description	(AL021687) cytochrome P450 [Arabidopsis thaliana]
Seq. No.	27938
Contig ID	164337_1.R1040
5'-most EST	zhf700958489.h1
Seq. No.	27939
Contig ID	164425_1.R1040
5'-most EST	jC-gmf102220093h03a1
Method	BLASTX
NCBI GI	g4220524
BLAST score	268
E value	2.0e-23
Match length	68
% identity	69
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]
Seq. No.	27940
Contig ID	164446_1.R1040
5'-most EST	vzy700752710.h1
Seq. No.	27941
Contig ID	164497_2.R1040
5'-most EST	vzy700753311.h1

Seq. No. 27956
 Contig ID 164683_1.R1040
 5'-most EST pmv700890195.h1
 Method BLASTX
 NCBI GI g2244792
 BLAST score 529
 E value 3.0e-54
 Match length 109
 % identity 86
 NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No. 27957
 Contig ID 164691_1.R1040
 5'-most EST leu701146647.h1

Seq. No. 27958
 Contig ID 164693_1.R1040
 5'-most EST pmv700890724.h1
 Method BLASTX
 NCBI GI g4220529
 BLAST score 349
 E value 8.0e-57
 Match length 144
 % identity 73
 NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 27959
 Contig ID 164705_1.R1040
 5'-most EST uC-gmflminsoy034g04b1

Seq. No. 27960
 Contig ID 164755_1.R1040
 5'-most EST fC-gmse700753182a1
 Method BLASTX
 NCBI GI g2833378
 BLAST score 652
 E value 2.0e-68
 Match length 194
 % identity 65
 NCBI Description HEXOKINASE >gi_619928 (U18754) hexokinase [Arabidopsis thaliana] >gi_1582383_prf_2118367A hexokinase [Arabidopsis thaliana]

Seq. No. 27961
 Contig ID 164774_1.R1040
 5'-most EST uC-gmropic106g09b1
 Method BLASTX
 NCBI GI g4325342
 BLAST score 354
 E value 1.0e-33
 Match length 121
 % identity 63
 NCBI Description (AF128393) No definition line found [Arabidopsis thaliana]

Seq. No. 27962
 Contig ID 164816_1.R1040

[illegible]

Seq. No.	27964
Contig ID	164835_1.R1040
5'-most EST	epx701108908.h1

Seq. No.	27966
Contig ID	164848_1.R1040
5'-most EST	vzy700753314.h1

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Seq. No.          27968
Contig ID         164876_1.R1040
5'-most EST      fC-gmse700753353a2
Method            BLASTX
NCBI GI           g2832304
BLAST score       189
E value           9.0e-15
Match length      60
% identity        58
NCBI Description  (AF044489) receptor-like protein kinase [Oryza sativa]
```


NCBI GI g1173063
 BLAST score 281
 E value 2.0e-25
 Match length 78
 % identity 71
 NCBI Description 60S RIBOSOMAL PROTEIN YL17-B >gi_1071989_pir_S56960
 ribosomal protein L17.e.B, cytosolic - yeast (Saccharomyces
 cerevisiae) >gi_1008376_emb_CAA89472_ (Z49452) ORF YJL177w
 [Saccharomyces cerevisiae]

Seq. No. 27993
 Contig ID 165255_1.R1040
 5'-most EST vzy700755902.h1

Seq. No. 27994
 Contig ID 165306_1.R1040
 5'-most EST leu701151074.h1
 Method BLASTX
 NCBI GI g1916809
 BLAST score 237
 E value 4.0e-20
 Match length 83
 % identity 61
 NCBI Description (U81163) auxin-binding protein [Prunus persica]

Seq. No. 27995
 Contig ID 165353_1.R1040
 5'-most EST fC-gmse700754105a1
 Method BLASTN
 NCBI GI g517257
 BLAST score 66
 E value 2.0e-28
 Match length 118
 % identity 89
 NCBI Description Z.mays MNB1a mRNA for DNA-binding protein

Seq. No. 27996
 Contig ID 165356_1.R1040
 5'-most EST jsh701066076.h1

Seq. No. 27997
 Contig ID 165376_1.R1040
 5'-most EST dpv701103230.h1
 Method BLASTX
 NCBI GI g4063743
 BLAST score 402
 E value 6.0e-39
 Match length 147
 % identity 58
 NCBI Description (AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No. 27998
 Contig ID 165427_1.R1040
 5'-most EST sat701007081.h1

Seq. No. 27999
 Contig ID 165432_1.R1040

5'-most EST vzy700756123.h1

Seq. No. 28000
 Contig ID 165434_1.R1040
 5'-most EST fC-gmse700754216a2
 Method BLASTX
 NCBI GI g3928095
 BLAST score 1029
 E value 1.0e-112
 Match length 258
 % identity 74
 NCBI Description (AC005770) putative protein kinase [Arabidopsis thaliana]

Seq. No. 28001
 Contig ID 165461_1.R1040
 5'-most EST sat701014070.h1
 Method BLASTX
 NCBI GI g3193306
 BLAST score 381
 E value 1.0e-36
 Match length 120
 % identity 67
 NCBI Description (AF069300) contains similarity to Arabidopsis
 membrane-associated salt-inducible-like protein
 (GB:AL021637) [Arabidopsis thaliana]

Seq. No. 28002
 Contig ID 165468_1.R1040
 5'-most EST asn701141825.h1
 Method BLASTN
 NCBI GI g3600062
 BLAST score 111
 E value 2.0e-55
 Match length 363
 % identity 83
 NCBI Description Arabidopsis thaliana BAC T25C13

Seq. No. 28003
 Contig ID 165486_1.R1040
 5'-most EST bth700845218.h1
 Method BLASTX
 NCBI GI g3114658
 BLAST score 234
 E value 2.0e-19
 Match length 108
 % identity 42
 NCBI Description (AF060871) hypothetical alcohol dehydrogenase [Rhodococcus
 rhodochrous]

Seq. No. 28004
 Contig ID 165486_2.R1040
 5'-most EST vzy700754292.h1
 Method BLASTN
 NCBI GI g2264306
 BLAST score 44
 E value 2.0e-15
 Match length 203

(HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 28020
 Contig ID 165758_1.R1040
 5'-most EST uC-gmflminsoy091g09b1
 Method BLASTN
 NCBI GI g1638836
 BLAST score 166
 E value 3.0e-88
 Match length 438
 % identity 84
 NCBI Description H.vulgare mRNA for alpha-tubulin

Seq. No. 28021
 Contig ID 165763_1.R1040
 5'-most EST jC-gmfl02220077b10a1
 Method BLASTX
 NCBI GI g3548808
 BLAST score 221
 E value 8.0e-18
 Match length 89
 % identity 54
 NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 28022
 Contig ID 165777_1.R1040
 5'-most EST vzy700754713.h1

Seq. No. 28023
 Contig ID 165788_1.R1040
 5'-most EST fC-gmse700754725a2
 Method BLASTX
 NCBI GI g584882
 BLAST score 380
 E value 1.0e-36
 Match length 131
 % identity 54
 NCBI Description CYCLOARTENOL SYNTHASE (2,3-EPOXYSQUALENE--CYCLOARTENOL CYCLASE) >gi_452446 (U02555) cycloartenol synthase; (S)-2,3-epoxysqualene mutase [Arabidopsis thaliana]

Seq. No. 28024
 Contig ID 165835_1.R1040
 5'-most EST asn701138122.h1

Seq. No. 28025
 Contig ID 165850_1.R1040
 5'-most EST jC-gmle01810086f01a1

Seq. No. 28026
 Contig ID 165853_1.R1040
 5'-most EST vzy700754816.h1
 Method BLASTX
 NCBI GI g3461848
 BLAST score 231
 E value 2.0e-19

Contig ID 166059_1.R1040
 5'-most EST uC-gmflminsoy028e09b1
 Method BLASTX
 NCBI GI g1263160
 BLAST score 331
 E value 2.0e-30
 Match length 217
 % identity 9
 NCBI Description (X89226) leucine-rich repeat/receptor protein kinase [Oryza sativa]

Seq. No. 28035
 Contig ID 166125_1.R1040
 5'-most EST vzy700755190.h1

Seq. No. 28036
 Contig ID 166176_1.R1040
 5'-most EST vzy700755267.h1
 Method BLASTN
 NCBI GI g1171481
 BLAST score 104
 E value 2.0e-51
 Match length 260
 % identity 85
 NCBI Description Nicotiana tabacum mRNA for nitrilase, complete cds

Seq. No. 28037
 Contig ID 166191_1.R1040
 5'-most EST fC-gmst700888672d3

Seq. No. 28038
 Contig ID 166206_1.R1040
 5'-most EST fC-gmse7000755316a1
 Method BLASTN
 NCBI GI g3860320
 BLAST score 215
 E value 1.0e-117
 Match length 475
 % identity 86
 NCBI Description Cicer arietinum mRNA for beta-galactosidase, clone CanBGal-5

Seq. No. 28039
 Contig ID 166216_1.R1040
 5'-most EST uC-gmrominsoy201h12b1
 Method BLASTX
 NCBI GI g1938424
 BLAST score 190
 E value 4.0e-14
 Match length 97
 % identity 49
 NCBI Description (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans]

Seq. No. 28040
 Contig ID 166229_1.R1040
 5'-most EST uC-gmrominsoy106g01b1

[illegible]

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Seq. No.      28068
Contig ID     166905_1.R1040
5'-most EST   hrw701063660.h1
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Seq. No.	28070
Contig ID	166918_1.R1040
5'-most EST	jC-qmf102220081b08a1

Seq. No.	28071
Contig ID	166923_1.R1040
5'-most EST	jC-qmst02400065a11d1

Seq. No.	28072
Contig ID	166927_1.R1040
5'-most EST	vzy700756461.h1

Seq. No.	28073
Contig ID	166960_1.R1040
5'-most EST	leu701147985.h1

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Seq. No.          28074
Contig ID         166976_1.R1040
5'-most EST      zhf700955028.h1
Method           BLASTX
NCBI GI          g3482978
BLAST score      277
E value          8.0e-25
Match length     108
% identity       61
NCBI Description  (AL031369) putative protein [Arabidopsis thaliana]
```


% identity	64
NCBI Description	(Y13632) dem [<i>Lycopersicon esculentum</i>]
Seq. No.	28088
Contig ID	167215_1.R1040
5'-most EST	euj700697912.h1
Seq. No.	28089
Contig ID	167220_1.R1040
5'-most EST	euj700697919.h1
Seq. No.	28090
Contig ID	167233_1.R1040
5'-most EST	zhf700957625.h1
Method	BLASTX
NCBI GI	g4467108
BLAST score	141
E value	9.0e-09
Match length	46
% identity	61
NCBI Description	(AL035538) hypothetical protein [<i>Arabidopsis thaliana</i>]
Seq. No.	28091
Contig ID	167238_1.R1040
5'-most EST	euj700697955.h1
Seq. No.	28092
Contig ID	167280_1.R1040
5'-most EST	euj700698032.h1
Method	BLASTX
NCBI GI	g2244807
BLAST score	175
E value	7.0e-13
Match length	73
% identity	53
NCBI Description	(Z97336) hypothetical protein [<i>Arabidopsis thaliana</i>]
Seq. No.	28093
Contig ID	167287_1.R1040
5'-most EST	uC-gmro ⁻ minsoy087b11b1
Method	BLASTX
NCBI GI	g3953471
BLAST score	322
E value	8.0e-30
Match length	122
% identity	52
NCBI Description	(AC002328) F22O2.16 [<i>Arabidopsis thaliana</i>]
Seq. No.	28094
Contig ID	167396_1.R1040
5'-most EST	crrh700851493.h1
Seq. No.	28095
Contig ID	167406_1.R1040
5'-most EST	zpv700757086.h1
Method	BLASTX
NCBI GI	q2507426

Contig ID	167556_1.R1040
5'-most EST	rlr700899695.h1
Method	BLASTX
NCBI GI	g4572676
BLAST score	316
E value	6.0e-29
Match length	187
% identity	36
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]
Seq. No.	28103
Contig ID	167611_1.R1040
5'-most EST	kl1701209728.h1
Seq. No.	28104
Contig ID	167613_1.R1040
5'-most EST	uC-gmronoir065c05b1
Seq. No.	28105
Contig ID	167641_1.R1040
5'-most EST	zpv700757524.h1
Seq. No.	28106
Contig ID	167673_1.R1040
5'-most EST	xpa700795867.h1
Seq. No.	28107
Contig ID	167692_1.R1040
5'-most EST	zpv700757614.h1
Method	BLASTX
NCBI GI	g3980413
BLAST score	364
E value	4.0e-35
Match length	94
% identity	16
NCBI Description	(AC004561) pumilio-like protein [Arabidopsis thaliana]
Seq. No.	28108
Contig ID	167727_1.R1040
5'-most EST	jC-gmle01810087a02d1
Seq. No.	28109
Contig ID	167745_1.R1040
5'-most EST	jC-gmro02910072e07a1
Seq. No.	28110
Contig ID	167756_1.R1040
5'-most EST	zpv700758462.h1
Method	BLASTX
NCBI GI	g1084950
BLAST score	195
E value	8.0e-15
Match length	143
% identity	29
NCBI Description	probable membrane protein YPR029c - yeast (Saccharomyces cerevisiae) >gi_809594_emb_CAA89283_(Z49274) unknown [Saccharomyces cerevisiae] >gi_1314103_emb_CAA95025_

(Z71255) unknown [Saccharomyces cerevisiae]

Seq. No. 28111
Contig ID 167774_1.R1040
5'-most EST fC-gmse7000757783f1
Method BLASTX
NCBI GI g1076755
BLAST score 537
E value 8.0e-76
Match length 175
% identity 79
NCBI Description protein kinase - rice >gi_450300 (L27821) protein kinase [Oryza sativa]

Seq. No. 28112
Contig ID 167806_1.R1040
5'-most EST zpv700757855.h1
Method BLASTX
NCBI GI g3212855
BLAST score 378
E value 5.0e-36
Match length 207
% identity 44
NCBI Description (AC004005) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28113
Contig ID 167840_1.R1040
5'-most EST zhf700958356.h1
Method BLASTX
NCBI GI g3831452
BLAST score 189
E value 5.0e-14
Match length 171
% identity 27
NCBI Description (AC005700) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 28114
Contig ID 167854_1.R1040
5'-most EST zhf700953487.h1

Seq. No. 28115
Contig ID 167860_1.R1040
5'-most EST zpv700757966.h1
Method BLASTX
NCBI GI g4467158
BLAST score 169
E value 7.0e-12
Match length 108
% identity 55
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 28116
Contig ID 167944_1.R1040
5'-most EST zpv700758128.h1

Seq. No. 28117
Contig ID 168079_1.R1040

0968-715X

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Seq. No.      28119
Contig ID     168114_1.R1040
5'-most EST  sat701002912.h1
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NCBI Description Soybean glycinin A-1a-B-x subunit mRNA, complete cds

Seq. No.	28122
Contig ID	168211_1.R1040
5'-most EST	zpv700758640.h1

Seq. No.	28123
Contig ID	168257_1.R1040
5'-most EST	zpv700758723.h1

Seq. No.	28124
Contig ID	168394_1.R1040
5'-most EST	zpv700759012.h1

Seq. No.	28125
Contig ID	168417_1.R1040
5'-most EST	zhf700955494.h1

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

4359

5'-most EST	zpv700761731.h1
Method	BLASTX
NCBI GI	g3790677
BLAST score	143
E value	6.0e-09
Match length	103
% identity	33
NCBI Description	(AF099002) similar to human 5'-nucleotidase (SW:P49902) [Caenorhabditis elegans]
Seq. No.	28154
Contig ID	169560_1.R1040
5'-most EST	uC-gmrominsoy029h01b1
Method	BLASTN
NCBI GI	g2924733
BLAST score	41
E value	2.0e-13
Match length	61
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]
Seq. No.	28155
Contig ID	169613_1.R1040
5'-most EST	zpv700762023.h1
Method	BLASTX
NCBI GI	g3372671
BLAST score	432
E value	6.0e-43
Match length	105
% identity	83
NCBI Description	(AF061286) gamma-adaptin 1 [Arabidopsis thaliana]
Seq. No.	28156
Contig ID	169680_1.R1040
5'-most EST	epx701110086.h1
Seq. No.	28157
Contig ID	169712_1.R1040
5'-most EST	jC-gmfl02220079g12a1
Seq. No.	28158
Contig ID	169719_1.R1040
5'-most EST	uC-gmflminsoy046h06b1
Method	BLASTN
NCBI GI	g975703
BLAST score	55
E value	6.0e-22
Match length	174
% identity	88
NCBI Description	P.sativum GR gene
Seq. No.	28159
Contig ID	169719_2.R1040
5'-most EST	epx701107025.h1
Method	BLASTN
NCBI GI	g975703

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Seq. No.	28175
Contig ID	170233_1.R1040
5'-most EST	jC-gmf102220092a11a1

Seq. No.	28177
Contig ID	170397_1.R1040
5'-most EST	zpv700763625.h1

Seq. No.	28179
Contig ID	170451_1.R1040
5'-most EST	jC-qmle01810094d11d1

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Seq. No.          28181
Contig ID         170486_1.R1040
5'-most EST      fC-gmrO700863840a3
Method            BLASTX
NCBI GI           g1743354
BLAST score       747
E value           1.0e-109
Match length      264
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0958-0167

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Seq. No.          28211
Contig ID         170954_1.R1040
5'-most EST      fC-gmro700865034a4
Method            BLASTX
NCBI GI           g4262226
BLAST score       246
E value           3.0e-20
Match length      166
% identity        39
NCBI Description  (AC006200) putative protein kinase [Arabidopsis thaliana]
```

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Seq. No.          28213
Contig ID         171025_1.R1040
5'-most EST      fC-gmro700865758a3
Method            BLASTX
NCBI GI           g1930081
BLAST score       556
E value           1.0e-56
Match length      247
% identity        53
NCBI Description  (U92878) acyl-ACP thioesterase [Garcinia mangostana]
```

Seq. No.	28215
Contig ID	171078_1.R1040
5'-most EST	zhf700957058.h1

4371

Match length 59
 % identity 78
 NCBI Description (AB017564) dof zinc finger protein [Arabidopsis thaliana]

Seq. No. 28231
 Contig ID 171401_1.R1040
 5'-most EST zsg701127091.h1
 Method BLASTX
 NCBI GI g729273
 BLAST score 432
 E value 7.0e-43
 Match length 111
 % identity 77
 NCBI Description CYPRO4 PROTEIN >gi_322804_pir_S28592 cypro4 protein -
 cardoon >gi_17959_emb_CAA49354_ (X69672) cypro4 [Cynara
 cardunculus]

Seq. No. 28232
 Contig ID 171422_1.R1040
 5'-most EST asn701136905.h1
 Method BLASTX
 NCBI GI g2829887
 BLAST score 164
 E value 2.0e-11
 Match length 105
 % identity 37
 NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 28233
 Contig ID 171429_1.R1040
 5'-most EST eep700865982.h1
 Method BLASTX
 NCBI GI g4314358
 BLAST score 400
 E value 4.0e-39
 Match length 110
 % identity 69
 NCBI Description (AC006340) putative kinesin heavy chain protein
 [Arabidopsis thaliana]

Seq. No. 28234
 Contig ID 171468_1.R1040
 5'-most EST awf700837144.h1

Seq. No. 28235
 Contig ID 171486_1.R1040
 5'-most EST fde700873229.h1

Seq. No. 28236
 Contig ID 171494_1.R1040
 5'-most EST eep700866113.h1
 Method BLASTX
 NCBI GI g3236253
 BLAST score 231
 E value 6.0e-19
 Match length 121
 % identity 47

Contig ID 171752_1.R1040
5'-most EST zhf700959861.h1

Seq. No. 28261
Contig ID 171753_1.R1040
5'-most EST zhf700958583.h1

Seq. No. 28262
Contig ID 171770_1.R1040
5'-most EST leu701156953.h1

Seq. No. 28263
Contig ID 171791_1.R1040
5'-most EST eep700866649.h1

Seq. No. 28264
Contig ID 171793_1.R1040
5'-most EST eep700866653.h1
Method BLASTX
NCBI GI g4454052
BLAST score 192
E value 8.0e-15
Match length 87
% identity 48
NCBI Description (AL035394) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28265
Contig ID 171819_1.R1040
5'-most EST eep700866701.h1

Seq. No. 28266
Contig ID 171855_1.R1040
5'-most EST fua701042719.h1
Method BLASTX
NCBI GI g4006829
BLAST score 673
E value 6.0e-71
Match length 145
% identity 88
NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No. 28267
Contig ID 171860_1.R1040
5'-most EST kl1701212235.h1

Seq. No. 28268
Contig ID 171875_1.R1040
5'-most EST leu701148609.h1
Method BLASTX
NCBI GI g3176707
BLAST score 157
E value 9.0e-11
Match length 86
% identity 42
NCBI Description (AC002392) putative proline-rich protein APG [Arabidopsis thaliana]

Seq. No. 28274
 Contig ID 171907_1.R1040
 5'-most EST jC-gmst02400073f11a1

Seq. No. 28275
 Contig ID 171908_1.R1040
 5'-most EST leu701146451.h1
 Method BLASTN
 NCBI GI g2143322
 BLAST score 42
 E value 2.0e-14
 Match length 82
 % identity 88
 NCBI Description P.deltoides chloroplast DNA for psbB operon

Seq. No. 28276
 Contig ID 171916_1.R1040
 5'-most EST sat701002934.h1
 Method BLASTX
 NCBI GI g2760830
 BLAST score 597
 E value 3.0e-62
 Match length 123
 % identity 88
 NCBI Description (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No. 28277
 Contig ID 171917_1.R1040
 5'-most EST pmv700891158.h1

Seq. No. 28278
 Contig ID 171929_1.R1040
 5'-most EST eep700867235.h1
 Method BLASTX
 NCBI GI g2346978
 BLAST score 147
 E value 1.0e-09
 Match length 74
 % identity 47
 NCBI Description (AB006601) ZPT2-14 [Petunia x hybrida]

Seq. No. 28279
 Contig ID 171930_1.R1040
 5'-most EST eep700867282.h1
 Method BLASTX
 NCBI GI g4038055
 BLAST score 261
 E value 5.0e-23
 Match length 88
 % identity 58
 NCBI Description (AC005897) putative cytochrome P450 [Arabidopsis thaliana]
 >gi_4557077_gb_AAD22516.1_AC007045_16 (AC007045) putative
 cytochrome p450 [Arabidopsis thaliana]

Seq. No. 28280

[illegible]

NCBI Description (AF128407) lipase homolog [Arabidopsis thaliana]

NCBI Description (X95738) proline transporter 2 [Arabidopsis thaliana]

Match length	17.4
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% identity	24
NCBI Description	(AC004261) putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]
Seq. No.	28290
Contig ID	172145_1.R1040
5'-most EST	dpv701097666.h1
Seq. No.	28291
Contig ID	172159_1.R1040
5'-most EST	eep700867465.h1
Method	BLASTX
NCBI GI	g4099833
BLAST score	162
E value	2.0e-11
Match length	77
% identity	42
NCBI Description	(U90265) bifunctional nuclease [Zinnia elegans]
Seq. No.	28292
Contig ID	172168_1.R1040
5'-most EST	eep700867487.h1
Seq. No.	28293
Contig ID	172173_1.R1040
5'-most EST	jC-gmf102220148c08a1
Method	BLASTX
NCBI GI	g4165861
BLAST score	536
E value	9.0e-55
Match length	164
% identity	29
NCBI Description	(AF006603) histone deacetylase mHDA2 [Mus musculus]
Seq. No.	28294
Contig ID	172181_1.R1040
5'-most EST	jC-gmro02910054a03d1
Seq. No.	28295
Contig ID	172192_1.R1040
5'-most EST	eep700867563.h1
Seq. No.	28296
Contig ID	172212_1.R1040
5'-most EST	asn701131028.h1
Method	BLASTX
NCBI GI	g3775999
BLAST score	291
E value	2.0e-26
Match length	66
% identity	82
NCBI Description	(AJ010463) RNA helicase [Arabidopsis thaliana]
Seq. No.	28297
Contig ID	172218_1.R1040
5'-most EST	eep700867656.h1

Seq. No. 28319
 Contig ID 172510_1.R1040
 5'-most EST eep700868455.h1

Seq. No. 28320
 Contig ID 172511_1.R1040
 5'-most EST zhf700965043.h1
 Method BLASTX
 NCBI GI g3329368
 BLAST score 326
 E value 2.0e-30
 Match length 103
 % identity 64
 NCBI Description (AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 28321
 Contig ID 172541_1.R1040
 5'-most EST zhf700961577.h1
 Method BLASTX
 NCBI GI g2583118
 BLAST score 227
 E value 4.0e-28
 Match length 105
 % identity 66
 NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28322
 Contig ID 172593_1.R1040
 5'-most EST sat701007218.h2

Seq. No. 28323
 Contig ID 172603_1.R1040
 5'-most EST eep700868417.h1
 Method BLASTX
 NCBI GI g3287695
 BLAST score 454
 E value 5.0e-84
 Match length 316
 % identity 56
 NCBI Description (AC003979) Similar to hypothetical protein C34B7.2
 gb_1729503 from C. elegans cosmid gb_283220. [Arabidopsis
 thaliana]

Seq. No. 28324
 Contig ID 172630_1.R1040
 5'-most EST dpv701097185.h1

Seq. No. 28325
 Contig ID 172645_1.R1040
 5'-most EST epx701104373.h1
 Method BLASTX
 NCBI GI g1710587
 BLAST score 194
 E value 3.0e-15
 Match length 53
 % identity 70
 NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P0 >gi_1196897 (L46848) acidic

5'-most EST eep700869140.h1
 Method BLASTX
 NCBI GI g3482917
 BLAST score 456
 E value 9.0e-71
 Match length 214
 % identity 69
 NCBI Description (AC003970) Similar to Glucose-6-phosphate dehydrogenases, gi_2276344, gi_2829880, gi_2352919 and others. [Arabidopsis thaliana]

Seq. No. 28351
 Contig ID 173013_1.R1040
 5'-most EST g5678068
 Method BLASTX
 NCBI GI g3367568
 BLAST score 272
 E value 3.0e-36
 Match length 117
 % identity 62
 NCBI Description (AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No. 28352
 Contig ID 173020_1.R1040
 5'-most EST eep700869182.h1

Seq. No. 28353
 Contig ID 173034_1.R1040
 5'-most EST leu701155874.h1
 Method BLASTX
 NCBI GI g2827631
 BLAST score 420
 E value 2.0e-41
 Match length 95
 % identity 85
 NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 28354
 Contig ID 173048_1.R1040
 5'-most EST uC-gmrominsoy093d04b1
 Method BLASTX
 NCBI GI g3193306
 BLAST score 403
 E value 2.0e-39
 Match length 116
 % identity 70
 NCBI Description (AF069300) contains similarity to Arabidopsis membrane-associated salt-inducible-like protein (GB:AL021637) [Arabidopsis thaliana]

Seq. No. 28355
 Contig ID 173065_1.R1040
 5'-most EST eep700869336.h1

Seq. No. 28356
 Contig ID 173085_1.R1040

Seq. No.	28370
Contig ID	173253_1.R1040
5'-most EST	eep700869735.h1
Method	BLASTX
NCBI GI	g4038043
BLAST score	174
E value	2.0e-12
Match length	100
% identity	37
NCBI Description	(AC005936) putative DNA-binding protein [Arabidopsis thaliana]
Seq. No.	28371
Contig ID	173289_1.R1040
5'-most EST	eep700869833.h1
Seq. No.	28372
Contig ID	173305_1.R1040
5'-most EST	jC-gmle01810049a03d1
Method	BLASTX
NCBI GI	g3176715
BLAST score	240
E value	4.0e-20
Match length	69
% identity	65
NCBI Description	(AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
Seq. No.	28373
Contig ID	173308_1.R1040
5'-most EST	zsg701124666.h1
Method	BLASTX
NCBI GI	g3687223
BLAST score	365
E value	7.0e-35
Match length	89
% identity	87
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]
Seq. No.	28374
Contig ID	173326_1.R1040
5'-most EST	xzm700763704.h1
Method	BLASTX
NCBI GI	g4467124
BLAST score	505
E value	2.0e-51
Match length	116
% identity	73
NCBI Description	(AL035538) hypothetical protein [Arabidopsis thaliana]
Seq. No.	28375
Contig ID	173342_1.R1040
5'-most EST	uC-gmropic101b04b1
Method	BLASTX
NCBI GI	g2388577
BLAST score	303

Seq. No. 28390
Contig ID 173557 1.R1040
5'-most EST g4260250

Seq. No. 28391
Contig ID 173593 1.R1040
5'-most EST eep700870382.h1

Seq. No. 28392
Contig ID 173615 1.R1040
5'-most EST eep700870429.h1

Seq. No. 28393
Contig ID 173622 1.R1040
5'-most EST eep700870441.h1
Method BLASTX
NCBI GI g112947
BLAST score 258
E value 2.0e-22
Match length 102
% identity 43
NCBI Description AAC-RICH MRNA CLONE AAC3 PROTEIN >gi_84121_pir_S05357
hypothetical protein (clone AAC3) - slime mold
(Dictyostelium discoideum) (fragment)
>gi_7176_emb_CAA34531 (X16524) coding region (AA 1 - 437)
[Dictyostelium discoideum]

Seq. No. 28394
Contig ID 173632 1.R1040
5'-most EST gsv701050008.h1
Method BLASTX
NCBI GI g2262177
BLAST score 530
E value 3.0e-54
Match length 138
% identity 70
NCBI Description (AC002329) hypothetical protein similar to T18A10.3
[Arabidopsis thaliana]

Seq. No. 28395
Contig ID 173661 1.R1040
5'-most EST zlv700807517.h1

Seq. No. 28396
Contig ID 173705 1.R1040
5'-most EST uC-gmropic042a04b1

Seq. No. 28397
Contig ID 173728 1.R1040
5'-most EST zlv700807612.h1
Method BLASTX
NCBI GI g3402758
BLAST score 428
E value 2.0e-45
Match length 152
% identity 62
NCBI Description (AL031187) serine/threonine kinase - like protein

[Arabidopsis thaliana]

Seq. No. 28398
 Contig ID 173787_1.R1040
 5'-most EST gsf700698326.h1
 Method BLASTX
 NCBI GI g3785989
 BLAST score 195
 E value 3.0e-15
 Match length 107
 % identity 48
 NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]

Seq. No. 28399
 Contig ID 173806_1.R1040
 5'-most EST gsf700698355.h1

Seq. No. 28400
 Contig ID 173821_1.R1040
 5'-most EST xpa700795033.h1

Seq. No. 28401
 Contig ID 173822_1.R1040
 5'-most EST jC-gmro02910016g07d1
 Method BLASTX
 NCBI GI g2262100
 BLAST score 314
 E value 8.0e-29
 Match length 71
 % identity 75
 NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 28402
 Contig ID 173829_1.R1040
 5'-most EST dpv701102034.h1
 Method BLASTX
 NCBI GI g2129635
 BLAST score 411
 E value 5.0e-40
 Match length 188
 % identity 50
 NCBI Description light repressible receptor protein kinase - Arabidopsis thaliana >gi_1321686_emb_CAA66376_(X97774) light repressible receptor protein kinase [Arabidopsis thaliana]

Seq. No. 28403
 Contig ID 173864_1.R1040
 5'-most EST fC-gmro700698445a1
 Method BLASTX
 NCBI GI g2224911
 BLAST score 225
 E value 3.0e-18
 Match length 145
 % identity 39
 NCBI Description (U93048) somatic embryogenesis receptor-like kinase [Daucus carota]

Seq. No. 28404
Contig ID 173878_1.R1040
5'-most EST gsf700698471.h1

Seq. No. 28405
Contig ID 173897_1.R1040
5'-most EST leu701150681.h1
Method BLASTX
NCBI GI g3947733
BLAST score 168
E value 3.0e-14
Match length 93
% identity 47
NCBI Description (AJ009719) NL25 [Solanum tuberosum]

Seq. No. 28406
Contig ID 173905_1.R1040
5'-most EST zsg701124722.h1

Seq. No. 28407
Contig ID 173912_1.R1040
5'-most EST uC-gmf1minsoy061a05b1
Method BLASTN
NCBI GI g4159706
BLAST score 37
E value 4.0e-11
Match length 192
% identity 85
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence [Arabidopsis thaliana]

Seq. No. 28408
Contig ID 174024_1.R1040
5'-most EST zhf700952960.h1

Seq. No. 28409
Contig ID 174026_1.R1040
5'-most EST uC-gmrominsoy198f01b1
Method BLASTN
NCBI GI g1370171
BLAST score 131
E value 2.0e-67
Match length 259
% identity 88
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB1X

Seq. No. 28410
Contig ID 174088_1.R1040
5'-most EST xpa700792630.h1

Seq. No. 28411
Contig ID 174089_1.R1040
5'-most EST bth700844710.h1
Method BLASTX
NCBI GI g3164222
BLAST score 288
E value 9.0e-26

Match length 90
 % identity 61
 NCBI Description (AB008518) RMA1 [Arabidopsis thaliana] >gi_4206205
 (AF071527) RMA1 RING zinc finger protein [Arabidopsis
 thaliana]

Seq. No. 28412
 Contig ID 174089_3.R1040
 5'-most EST xpa700792631.h1

Seq. No. 28413
 Contig ID 174096_1.R1040
 5'-most EST uC-gmflminsoy097f12b1
 Method BLASTX
 NCBI GI g2909781
 BLAST score 234
 E value 1.0e-38
 Match length 118
 % identity 71
 NCBI Description (AF020288) MgATP-energized glutathione S-conjugate pump
 [Arabidopsis thaliana]

Seq. No. 28414
 Contig ID 174107_1.R1040
 5'-most EST g5606668
 Method BLASTX
 NCBI GI g2505877
 BLAST score 323
 E value 8.0e-30
 Match length 195
 % identity 42
 NCBI Description (Y12776) dehydrogenase [Arabidopsis thaliana]

Seq. No. 28415
 Contig ID 174146_1.R1040
 5'-most EST xpa700797244.h1

Seq. No. 28416
 Contig ID 174147_1.R1040
 5'-most EST xpa700792742.h1

Seq. No. 28417
 Contig ID 174192_1.R1040
 5'-most EST jC-gmro02910049a02a1

Seq. No. 28418
 Contig ID 174194_1.R1040
 5'-most EST jC-gmle01810094g03a1
 Method BLASTX
 NCBI GI g4092774
 BLAST score 268
 E value 2.0e-23
 Match length 134
 % identity 43
 NCBI Description (AF105140) disease resistance gene homolog 9N [Brassica
 napus]

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5'-most EST k11701212438.h1
 Method BLASTX
 NCBI GI g3075397
 BLAST score 169
 E value 1.0e-11
 Match length 133
 % identity 34
 NCBI Description (AC004484) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28435
 Contig ID 174390_1.R1040
 5'-most EST hrw701063062.h1

Seq. No. 28436
 Contig ID 174403_1.R1040
 5'-most EST xpa700793202.h1

Seq. No. 28437
 Contig ID 174423_1.R1040
 5'-most EST xpa700793236.h1
 Method BLASTX
 NCBI GI g2511715
 BLAST score 682
 E value 6.0e-72
 Match length 175
 % identity 74
 NCBI Description (AF019380) putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]

Seq. No. 28438
 Contig ID 174436_1.R1040
 5'-most EST xpa700793265.h1

Seq. No. 28439
 Contig ID 174452_1.R1040
 5'-most EST xpa700793295.h1
 Method BLASTX
 NCBI GI g4097522
 BLAST score 317
 E value 5.0e-29
 Match length 131
 % identity 51
 NCBI Description (U63534) cinnamyl alcohol dehydrogenase [Fragaria x ananassa]

Seq. No. 28440
 Contig ID 174452_2.R1040
 5'-most EST jC-gmfl02220091a11a1
 Method BLASTX
 NCBI GI g4097522
 BLAST score 204
 E value 5.0e-16
 Match length 68
 % identity 62
 NCBI Description (U63534) cinnamyl alcohol dehydrogenase [Fragaria x ananassa]

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Seq. No. 28441
Contig ID 174467_1.R1040
5'-most EST jC-gmst02400011f04a1

Seq. No. 28442
Contig ID 174470_1.R1040
5'-most EST jC-gmle01810086a06a1
Method BLASTX
NCBI GI g2598573
BLAST score 161
E value 8.0e-11
Match length 89
% identity 43
NCBI Description (Y15292) MtN26 [Medicago truncatula]

Seq. No. 28443
Contig ID 174474_1.R1040
5'-most EST leu701148768.h1

Seq. No. 28444
Contig ID 174490_1.R1040
5'-most EST xpa700794557.h1

Seq. No. 28445
Contig ID 174499_1.R1040
5'-most EST uC-gmropic019g08b1

Seq. No. 28446
Contig ID 174501_1.R1040
5'-most EST jC-gmle01810087a06a1
Method BLASTX
NCBI GI g2208988
BLAST score 392
E value 6.0e-38
Match length 91
% identity 75
NCBI Description (Y10117) signal recognition particle subunit 9 [Zea mays]

Seq. No. 28447
Contig ID 174582_1.R1040
5'-most EST xpa700793537.h1

Seq. No. 28448
Contig ID 174593_1.R1040
5'-most EST xpa700793551.h1

Seq. No. 28449
Contig ID 174641_1.R1040
5'-most EST xpa700793647.h1

Seq. No. 28450
Contig ID 174654_1.R1040
5'-most EST pmv700892326.h1

Seq. No. 28451
Contig ID 174654_2.R1040
5'-most EST uC-gmflminsoy062e06b1

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Seq. No. 28467
 Contig ID 175057 1.R1040
 5'-most EST xpa700794496.h1

Seq. No. 28468
 Contig ID 175077 1.R1040
 5'-most EST dpv701099318.h1
 Method BLASTX
 NCBI GI g2130024
 BLAST score 332
 E value 5.0e-31
 Match length 111
 % identity 58
 NCBI Description DNA-binding protein ABF2 - wild oat
 >gi_1159879_emb_CAA88331_ (Z48431) DNA-binding protein
 [Avena fatua]

Seq. No. 28469
 Contig ID 175084 1.R1040
 5'-most EST bth700847836.h1

Seq. No. 28470
 Contig ID 175086 1.R1040
 5'-most EST xpa700794548.h1

Seq. No. 28471
 Contig ID 175093 1.R1040
 5'-most EST crh700854472.h1

Seq. No. 28472
 Contig ID 175100 1.R1040
 5'-most EST dpv701103314.h1

Seq. No. 28473
 Contig ID 175108 1.R1040
 5'-most EST hrw701059917.h1
 Method BLASTX
 NCBI GI g2134385
 BLAST score 638
 E value 1.0e-66
 Match length 170
 % identity 69
 NCBI Description protein kinase - chicken >gi_571460 (U16656) protein kinase
 [Gallus gallus]

Seq. No. 28474
 Contig ID 175127 1.R1040
 5'-most EST xpa700794634.h1
 Method BLASTX
 NCBI GI g2570342
 BLAST score 355
 E value 4.0e-34
 Match length 91
 % identity 69
 NCBI Description (U90929) glyoxalase II cytoplasmic isozyme [Arabidopsis
 thaliana]

Seq. No. 28475
Contig ID 175129_1.R1040
5'-most EST uC-gmropic098a10b1

Seq. No. 28476
Contig ID 175140_1.R1040
5'-most EST fde700873132.h1
Method BLASTX
NCBI GI g3068717
BLAST score 424
E value 5.0e-42
Match length 98
% identity 79
NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No. 28477
Contig ID 175147_1.R1040
5'-most EST jC-gmst02400030h07a1
Method BLASTX
NCBI GI g1669591
BLAST score 520
E value 1.0e-52
Match length 155
% identity 63
NCBI Description (D88742) O-methyltransferase [Glycyrrhiza echinata]

Seq. No. 28478
Contig ID 175151_1.R1040
5'-most EST zzp700831230.h1

Seq. No. 28479
Contig ID 175199_1.R1040
5'-most EST xpa700794766.h1
Method BLASTX
NCBI GI g1388078
BLAST score 191
E value 9.0e-15
Match length 62
% identity 52
NCBI Description (U35826) thioredoxin h [Arabidopsis thaliana]

Seq. No. 28480
Contig ID 175230_1.R1040
5'-most EST xpa700794824.h1
Method BLASTX
NCBI GI g2961348
BLAST score 271
E value 3.0e-24
Match length 83
% identity 57
NCBI Description (AL022140) putative protein [Arabidopsis thaliana]

Seq. No. 28481
Contig ID 175270_1.R1040
5'-most EST xpa700795083.h1

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NCBI GI	g3242708
BLAST score	404
E value	3.0e-39
Match length	196
% identity	45
NCBI Description	(AC003040) putative serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	28523
Contig ID	176133_1.R1040
5'-most EST	xpa700797096.h1
Method	BLASTX
NCBI GI	g3822223
BLAST score	543
E value	1.0e-55
Match length	141
% identity	69
NCBI Description	(AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]
Seq. No.	28524
Contig ID	176158_1.R1040
5'-most EST	xpa700796894.h1
Seq. No.	28525
Contig ID	176166_1.R1040
5'-most EST	g4306800
Method	BLASTX
NCBI GI	g3258575
BLAST score	672
E value	2.0e-70
Match length	279
% identity	54
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	28526
Contig ID	176215_1.R1040
5'-most EST	uC-gmrominsoyl65g09b1
Seq. No.	28527
Contig ID	176231_1.R1040
5'-most EST	xpa700797085.h1
Method	BLASTX
NCBI GI	g4006896
BLAST score	178
E value	8.0e-13
Match length	131
% identity	37
NCBI Description	(Z99708) SCARECROW-like protein [Arabidopsis thaliana]
Seq. No.	28528
Contig ID	176287_1.R1040
5'-most EST	zsg701117806.h2
Method	BLASTX
NCBI GI	g434759
BLAST score	1130
E value	1.0e-124

E value 2.0e-10
 Match length 47
 % identity 68
 NCBI Description (AB004871) CPC [Arabidopsis thaliana]
 >gi_4559383_gb_AAD23043.1_AC006526_8 (AC006526) putative
 DNA binding protein CPC [Arabidopsis thaliana]

Seq. No. 28536
 Contig ID 176528_1.R1040
 5'-most EST jC-gmst02400004c12d1

Seq. No. 28537
 Contig ID 176570_1.R1040
 5'-most EST xpa700797851.h1
 Method BLASTX
 NCBI GI g3033391
 BLAST score 284
 E value 7.0e-26
 Match length 78
 % identity 72
 NCBI Description (AC004238) putative amino acid transporter [Arabidopsis thaliana]

Seq. No. 28538
 Contig ID 176584_1.R1040
 5'-most EST dpv701097015.h1
 Method BLASTX
 NCBI GI g3941524
 BLAST score 299
 E value 2.0e-27
 Match length 68
 % identity 76
 NCBI Description (AF062916) putative transcription factor [Arabidopsis thaliana]

Seq. No. 28539
 Contig ID 176611_1.R1040
 5'-most EST xpa700797933.h1

Seq. No. 28540
 Contig ID 176614_1.R1040
 5'-most EST xpa700797938.h1
 Method BLASTX
 NCBI GI g2894600
 BLAST score 162
 E value 3.0e-11
 Match length 81
 % identity 36
 NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 28541
 Contig ID 176739_1.R1040
 5'-most EST uC-gmronoir062h08b1

Seq. No. 28542
 Contig ID 176784_1.R1040
 5'-most EST xpa700798275.h1

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Seq. No. 28591
Contig ID 177566_1.R1040
5'-most EST rca700997214.h1

Seq. No. 28592
Contig ID 177570_1.R1040
5'-most EST g5606878
Method BLASTX
NCBI GI g4468817
BLAST score 241
E value 2.0e-20
Match length 115
% identity 45
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 28593
Contig ID 177592_1.R1040
5'-most EST jC-gmle01810093c05a1

Seq. No. 28594
Contig ID 177598_1.R1040
5'-most EST rca700997269.h1
Method BLASTX
NCBI GI g1929056
BLAST score 219
E value 3.0e-18
Match length 75
% identity 59
NCBI Description (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]

Seq. No. 28595
Contig ID 177607_1.R1040
5'-most EST g5677865

Seq. No. 28596
Contig ID 177623_1.R1040
5'-most EST jC-gmro02910038a03a1
Method BLASTX
NCBI GI g4314363
BLAST score 376
E value 5.0e-36
Match length 179
% identity 42
NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 28597
Contig ID 177631_1.R1040
5'-most EST uC-gmropic091e09b1

Seq. No. 28598
Contig ID 177673_1.R1040
5'-most EST jex700906354.h1

Seq. No. 28599
Contig ID 177684_1.R1040
5'-most EST rca700997413.h1

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Method	BLASTX
NCBI GI	g2827552
BLAST score	202
E value	2.0e-28
Match length	76
% identity	75
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]
Seq. No.	28633
Contig ID	178365_1.R1040
5'-most EST	fC-gmse700655491d4
Seq. No.	28634
Contig ID	178381_1.R1040
5'-most EST	rca700998483.h1
Seq. No.	28635
Contig ID	178425_1.R1040
5'-most EST	uC-gmrominsoy139c02b1
Seq. No.	28636
Contig ID	178428_1.R1040
5'-most EST	asn701133668.h2
Method	BLASTX
NCBI GI	g3850588
BLAST score	147
E value	4.0e-09
Match length	315
% identity	27
NCBI Description	(AC005278) Contains similarity to gb_AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF_00168. ESTs gb_AA585988 and gb_T04384 come from this gene. [Arabidopsis thaliana]
Seq. No.	28637
Contig ID	178465_1.R1040
5'-most EST	zhf700964765.h1
Seq. No.	28638
Contig ID	178470_1.R1040
5'-most EST	g5677023
Seq. No.	28639
Contig ID	178500_1.R1040
5'-most EST	uC-gmflminsoy022b11b1
Seq. No.	28640
Contig ID	178504_1.R1040
5'-most EST	jC-gmle01810067g05a1
Seq. No.	28641
Contig ID	178525_1.R1040
5'-most EST	zhf700961951.h1
Seq. No.	28642
Contig ID	178532_1.R1040
5'-most EST	rca700998705.h1

5'-most EST	rca700998922.h1
Seq. No.	28650
Contig ID	178648_1.R1040
5'-most EST	kl1701210150.h1
Seq. No.	28651
Contig ID	178688_1.R1040
5'-most EST	rca700998964.h1
Seq. No.	28652
Contig ID	178742_1.R1040
5'-most EST	uC-gmrominsoy250f08b1
Method	BLASTN
NCBI GI	g2055227
BLAST score	46
E value	1.0e-16
Match length	66
% identity	92
NCBI Description	Glycine max mRNA for SRC1, complete cds
Seq. No.	28653
Contig ID	178799_1.R1040
5'-most EST	rca700999148.h1
Seq. No.	28654
Contig ID	178831_1.R1040
5'-most EST	fC-gmse700660737g3
Seq. No.	28655
Contig ID	178843_1.R1040
5'-most EST	rca700999269.h1
Seq. No.	28656
Contig ID	178862_1.R1040
5'-most EST	rca700999302.h1
Seq. No.	28657
Contig ID	178874_1.R1040
5'-most EST	zhf700952248.h1
Seq. No.	28658
Contig ID	178932_1.R1040
5'-most EST	rca700999506.h1
Seq. No.	28659
Contig ID	178950_1.R1040
5'-most EST	jC-gmfl02220077g11d1
Seq. No.	28660
Contig ID	178969_1.R1040
5'-most EST	zhf700962302.h1
Seq. No.	28661
Contig ID	179028_1.R1040
5'-most EST	zsq701124449.h1
Method	BLASTX

NCBI GI g2832717
 BLAST score 672
 E value 7.0e-71
 Match length 139
 % identity 89
 NCBI Description (AJ003114) alkaline/neutral invertase [*Lolium temulentum*]

Seq. No. 28686
 Contig ID 179589_1.R1040
 5'-most EST rca701000848.h1

Seq. No. 28687
 Contig ID 179595_1.R1040
 5'-most EST uC-gmropic037b06b1

Seq. No. 28688
 Contig ID 179606_1.R1040
 5'-most EST rca701001387.h1
 Method BLASTX
 NCBI GI g4102839
 BLAST score 749
 E value 9.0e-80
 Match length 172
 % identity 76
 NCBI Description (AF016713) LeOPT1 [*Lycopersicon esculentum*]

Seq. No. 28689
 Contig ID 179609_1.R1040
 5'-most EST rca701000785.h1

Seq. No. 28690
 Contig ID 179610_1.R1040
 5'-most EST g5605841

Seq. No. 28691
 Contig ID 179612_1.R1040
 5'-most EST hrw701062674.h1

Seq. No. 28692
 Contig ID 179613_1.R1040
 5'-most EST sat701003330.h1

Seq. No. 28693
 Contig ID 179626_1.R1040
 5'-most EST jex700904934.h1

Seq. No. 28694
 Contig ID 179632_1.R1040
 5'-most EST rca701000817.h1

Seq. No. 28695
 Contig ID 179642_1.R1040
 5'-most EST rca701000831.h1

Seq. No. 28696
 Contig ID 179666_1.R1040
 5'-most EST rca701000858.h1

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Seq. No.          28699
Contig ID         179738_1.R1040
5'-most EST      uC-gmröpic092f12b1
Method            BLASTX
NCBI GI           g1657621
BLAST score       362
E value           1.0e-34
Match length      97
% identity        66
NCBI Description  (U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236)
                  putative acyl-coA dehydrogenase [Arabidopsis thaliana]
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Seq. No.          28700
Contig ID         179742_1.R1040
5'-most EST      rca701000981.h1
Method            BLASTX
NCBI GI           g3005576
BLAST score       298
E value           6.0e-27
Match length      103
% identity        55
NCBI Description  (AF047718) putative high affinity nitrate transporter;
                  GmNRT2 [Glycine max]
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Seq. No.          28701
Contig ID         179757_1.R1040
5'-most EST      rca701001007.h1
Method            BLASTX
NCBI GI           g3218550
BLAST score       147
E value           2.0e-09
Match length      74
% identity        41
NCBI Description  (AB009399) Cdk-activating kinase 1At [Arabidopsis thaliana]
```

Seq. No.	28702
Contig ID	179769_1.R1040
5'-most EST	rca701001068.h1

Seq. No.	28703
Contig ID	179791 1.R1040

0001016 91048960

Contig ID 179889_1.R1040
5'-most EST rca701001167.h1

Seq. No. 28711
Contig ID 179912_1.R1040
5'-most EST rca701001195.h1
Method BLASTX
NCBI GI g228403
BLAST score 277
E value 6.0e-25
Match length 83
% identity 65
NCBI Description glycolate oxidase [Lens culinaris]

Seq. No. 28712
Contig ID 179913_1.R1040
5'-most EST rca701001675.h1
Method BLASTN
NCBI GI g12137
BLAST score 90
E value 5.0e-43
Match length 196
% identity 89
NCBI Description Pea chloroplast DNA (4.7 kb) 5' to ATP-synthase a subunit gene

Seq. No. 28713
Contig ID 179957_1.R1040
5'-most EST rca701001268.h1
Method BLASTX
NCBI GI g4098582
BLAST score 162
E value 4.0e-11
Match length 116
% identity 39
NCBI Description (U79567) RBM1 [Sminthopsis macroura]

Seq. No. 28714
Contig ID 179983_1.R1040
5'-most EST rca701001303.h1

Seq. No. 28715
Contig ID 179999_1.R1040
5'-most EST rca701001322.h1

Seq. No. 28716
Contig ID 180001_1.R1040
5'-most EST rca701001395.h1

Seq. No. 28717
Contig ID 180010_1.R1040
5'-most EST uC-gmrominsoy043b11b1

Seq. No. 28718
Contig ID 180025_1.R1040
5'-most EST rca701001353.h1
Method BLASTX

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NCBI GI	g2252840
BLAST score	157
E value	8.0e-11
Match length	83
% identity	39
NCBI Description	(AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]
Seq. No.	28768
Contig ID	180844_1.R1040
5'-most EST	fde700870511.h1
Seq. No.	28769
Contig ID	180850_1.R1040
5'-most EST	fC-gmst700889683f3
Method	BLASTX
NCBI GI	g128195
BLAST score	187
E value	1.0e-13
Match length	110
% identity	38
NCBI Description	NITRATE REDUCTASE (NR) >gi_66203_pir_RDTONH nitrate reductase (NADH) (EC 1.6.6.1) - tomato >gi_19283_emb_CAA32218_(X14060) nitrate reductase [Lycopersicon esculentum]
Seq. No.	28770
Contig ID	180866_1.R1040
5'-most EST	fde700870539.h1
Seq. No.	28771
Contig ID	180872_1.R1040
5'-most EST	fde700872774.h1
Seq. No.	28772
Contig ID	180886_1.R1040
5'-most EST	fde700870562.h1
Seq. No.	28773
Contig ID	180912_1.R1040
5'-most EST	fde700870606.h1
Seq. No.	28774
Contig ID	180917_1.R1040
5'-most EST	fde700870769.h1
Seq. No.	28775
Contig ID	180978_1.R1040
5'-most EST	fde700870695.h1
Method	BLASTX
NCBI GI	g1800147
BLAST score	277
E value	2.0e-24
Match length	71
% identity	76
NCBI Description	(U83655) membrane associated protein [Arabidopsis thaliana]

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Seq. No.	28786
Contig ID	181110_1.R1040
5'-most EST	fde700870873.h1

Seq. No.	28788
Contig ID	181117_2.R1040
5'-most EST	uC-qmrnoir038a08b1

Seq. No.	28790
Contig ID	181127_1.R1040
5'-most EST	fde700871025.h1

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Seq. No.          28791
Contig ID         181144_1.R1040
5'-most EST      hrw701061362.h1
Method            BLASTX
NCBI GI           g2792155
BLAST score       562
E value           1.0e-57
Match length      179
% identity        60
NCBI Description  (AJ223291) chalcone reductase [Sesbania rostrata]
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Seq. No.          28792
Contig ID         181148_1.R1040
5'-most EST      fde700870931.h1
Method            BLASTX
NCBI GI           g4375833
BLAST score       969
E value           1.0e-105
Match length      318
% identity        60
NCBI Description  (AL021713) receptor serine/threonine kinase-like protein
                  [Arabidopsis thaliana]
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% identity 52
 NCBI Description (AC002411) Contains similarity to neural cell adhesion molecule 2, large isoform precursor gb_M76710 from *Xenopus laevis*, and beta transducin from *S. cerevisiae* gb_Q05946. ESTs gb_N65081 gb_Z30910, gb_Z34190, gb_Z34611, gb_R30101, gb_H3630

Seq. No. 28794
 Contig ID 181156_1.R1040
 5'-most EST fde700870946.h1
 Method BLASTX
 NCBI GI g2642448
 BLAST score 282
 E value 1.0e-25
 Match length 79
 % identity 38
 NCBI Description (AC002391) hypothetical protein [*Arabidopsis thaliana*] >gi_3169187 (AC004401) hypothetical protein [*Arabidopsis thaliana*]

Seq. No. 28795
 Contig ID 181158_1.R1040
 5'-most EST uC-gmrominsoy080e12b1
 Method BLASTN
 NCBI GI g2264321
 BLAST score 46
 E value 1.0e-16
 Match length 94
 % identity 42
 NCBI Description *Arabidopsis thaliana* genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [*Arabidopsis thaliana*]

Seq. No. 28796
 Contig ID 181204_1.R1040
 5'-most EST fde700871020.h1
 Method BLASTX
 NCBI GI g3550554
 BLAST score 373
 E value 3.0e-36
 Match length 84
 % identity 82
 NCBI Description (Y17469) sarco/endoplasmic reticulum Ca²⁺ -ATPase [*Paramecium tetraurelia*]

Seq. No. 28797
 Contig ID 181232_1.R1040
 5'-most EST uC-gmropic026c02b1
 Method BLASTX
 NCBI GI g2262105
 BLAST score 323
 E value 7.0e-30
 Match length 96
 % identity 64
 NCBI Description (AC002343) unknown protein [*Arabidopsis thaliana*]

Seq. No. 28798
 Contig ID 181273_1.R1040

5'-most EST fde700871115.h1

Seq. No. 28799
 Contig ID 181302_1.R1040
 5'-most EST fde700871158.h1
 Method BLASTX
 NCBI GI g2832629
 BLAST score 176
 E value 1.0e-12
 Match length 115
 % identity 37
 NCBI Description (AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]

Seq. No. 28800
 Contig ID 181320_1.R1040
 5'-most EST g5677137
 Method BLASTN
 NCBI GI g3046710
 BLAST score 320
 E value 1.0e-180
 Match length 468
 % identity 92
 NCBI Description Cicer arietinum mRNA for replication factor C/activator 1 subunit, partial

Seq. No. 28801
 Contig ID 181375_1.R1040
 5'-most EST fde700871370.h1

Seq. No. 28802
 Contig ID 181378_1.R1040
 5'-most EST fde700871384.h1

Seq. No. 28803
 Contig ID 181380_1.R1040
 5'-most EST fde700871475.h1

Seq. No. 28804
 Contig ID 181406_1.R1040
 5'-most EST fde700875863.h1
 Method BLASTX
 NCBI GI g421842
 BLAST score 263
 E value 6.0e-31
 Match length 86
 % identity 81
 NCBI Description potassium channel protein - Arabidopsis thaliana >gi_166774 (M86990) potassium channel protein [Arabidopsis thaliana] >gi_1065906 (U25088) potassium channel protein [Arabidopsis thaliana]

Seq. No. 28805
 Contig ID 181414_1.R1040
 5'-most EST fde700872880.h1

Seq. No. 28806

Contig ID 181441_1.R1040
5'-most EST fde700871614.h1

Seq. No. 28807
Contig ID 181446_1.R1040
5'-most EST fde700873667.h1

Seq. No. 28808
Contig ID 181448_1.R1040
5'-most EST jex700909437.h1

Seq. No. 28809
Contig ID 181457_1.R1040
5'-most EST zzp700831121.h1
Method BLASTX
NCBI GI g1706884
BLAST score 365
E value 2.0e-34
Match length 276
% identity 34
NCBI Description FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR
(FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS)

Seq. No. 28810
Contig ID 181461_1.R1040
5'-most EST fde700875886.h1

Seq. No. 28811
Contig ID 181486_1.R1040
5'-most EST fde700875642.h1
Method BLASTX
NCBI GI g4567263
BLAST score 366
E value 2.0e-35
Match length 84
% identity 81
NCBI Description (AC006841) putative cell division inhibitor [Arabidopsis
thaliana]

Seq. No. 28812
Contig ID 181510_1.R1040
5'-most EST bth700845762.h1

Seq. No. 28813
Contig ID 181514_1.R1040
5'-most EST hrw701063367.h1

Seq. No. 28814
Contig ID 181541_1.R1040
5'-most EST asn701136708.h1
Method BLASTX
NCBI GI g4490317
BLAST score 380
E value 2.0e-36
Match length 188
% identity 43
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

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[illegible]

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Seq. No.          28844
Contig ID         182050_1.R1040
5'-most EST      fde700872717.h1
Method            BLASTN
NCBI GI           g1134881
BLAST score       118
E value           7.0e-60
Match length      262
% identity        86
NCBI Description  P.sativum mRNA for cysteine protease
```

```
Seq. No.          28845
Contig ID         182065_1.R1040
5'-most EST      sat701015446.h1
Method            BLASTX
NCBI GI           g2129820
BLAST score       190
E value           9.0e-15
Match length      82
% identity        49
NCBI Description  chitinase (EC 3.2.1.14) class II - peanut
                  >gi_1237025_emb_CAA57773_ (X82329) chitinase (class II)
                  [Arachis hypogaea]
```

Seq. No.	28846
Contig ID	182066_1.R1040
5'-most EST	fde700872743.h1

Seq. No.	28847
Contig ID	182067_1.R1040
5'-most EST	fde700875456.h1

```
Seq. No.      28848
Contig ID     182077_1.R1040
5'-most EST   fde700872757.h1
```

```
Seq. No.          28849
Contig ID         182078_1.R1040
5'-most EST      jC-gmr002910008g10a1
Method            BLASTX
NCBI GI           g3877656
BLAST score       324
E value           8.0e-30
Match length      203
```


% identity 21
 NCBI Description (Z72511) similar to nucleotide translocator [Caenorhabditis elegans]

Seq. No. 28850
 Contig ID 182078_2.R1040
 5'-most EST fde700872758.h1
 Method BLASTN
 NCBI GI g3510339
 BLAST score 36
 E value 6.0e-11
 Match length 96
 % identity 84
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No. 28851
 Contig ID 182078_3.R1040
 5'-most EST leu701156558.h1
 Method BLASTN
 NCBI GI g3510339
 BLAST score 32
 E value 1.0e-08
 Match length 96
 % identity 83
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No. 28852
 Contig ID 182079_1.R1040
 5'-most EST fde700875724.h1
 Method BLASTX
 NCBI GI g4063746
 BLAST score 221
 E value 4.0e-18
 Match length 85
 % identity 57
 NCBI Description (AC005851) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 28853
 Contig ID 182131_1.R1040
 5'-most EST uC-gmrominsoyl95e05b1
 Method BLASTX
 NCBI GI g2765817
 BLAST score 493
 E value 1.0e-49
 Match length 214
 % identity 47
 NCBI Description (Z95352) AtMlo-h1 [Arabidopsis thaliana]
 >gi_3892049_gb_AAC78258.1_AAC78258 (AC002330) AtMlo-h1 [Arabidopsis thaliana]

Seq. No. 28854
 Contig ID 182141_1.R1040
 5'-most EST g5058057

Seq. No. 28855

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Seq. No. 28875

[illegible][illegible][illegible][illegible][illegible][illegible]

NCBI GI g4490317
BLAST score 228
E value 1.0e-18
Match length 100
% identity 44
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 28909
Contig ID 182945_1.R1040
5'-most EST fde700874024.h1

Seq. No. 28910
Contig ID 182948_1.R1040
5'-most EST dpv701099247.h1
Method BLASTN
NCBI GI g2342717
BLAST score 52
E value 2.0e-20
Match length 80
% identity 91
NCBI Description Arabidopsis thaliana chromosome II BAC T14G11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 28911
Contig ID 183009_1.R1040
5'-most EST jC-gmle01810025e05a1

Seq. No. 28912
Contig ID 183014_1.R1040
5'-most EST jsh701069970.h2
Method BLASTX
NCBI GI g1279640
BLAST score 449
E value 1.0e-44
Match length 126
% identity 66
NCBI Description (X92204) NAM [Petunia x hybrida]

Seq. No. 28913
Contig ID 183027_1.R1040
5'-most EST fde700874161.h1

Seq. No. 28914
Contig ID 183032_1.R1040
5'-most EST epx701107729.h1

Seq. No. 28915
Contig ID 183069_1.R1040
5'-most EST zsg701118022.h2

Seq. No. 28916
Contig ID 183074_1.R1040
5'-most EST fua701037884.h1
Method BLASTX
NCBI GI g2827637
BLAST score 141
E value 1.0e-08

Seq. No. 28948
Contig ID 183615_1.R1040
5'-most EST leu701155293.h1

Seq. No. 28949
Contig ID 183624_1.R1040
5'-most EST fua701037786.h1

Seq. No. 28950
Contig ID 183631_1.R1040
5'-most EST jC-gmle01810094e07a1
Method BLASTN
NCBI GI g868002
BLAST score 122
E value 4.0e-62
Match length 338
% identity 84
NCBI Description Pumpkin mRNA for aconitase, complete cds

Seq. No. 28951
Contig ID 183638_1.R1040
5'-most EST fde700875021.h1

Seq. No. 28952
Contig ID 183646_1.R1040
5'-most EST fde700875129.h1
Method BLASTN
NCBI GI g1235600
BLAST score 154
E value 2.0e-81
Match length 234
% identity 92
NCBI Description S.macrospora EF1-alpha gene

Seq. No. 28953
Contig ID 183651_1.R1040
5'-most EST fde700875216.h1

Seq. No. 28954
Contig ID 183665_1.R1040
5'-most EST sat701011418.h1

Seq. No. 28955
Contig ID 183677_1.R1040
5'-most EST zhf700958916.h1
Method BLASTX
NCBI GI g1076365
BLAST score 170
E value 8.0e-12
Match length 184
% identity 29
NCBI Description pectinesterase (EC 3.1.1.11) PME1 precursor - Arabidopsis thaliana >gi_2129666_pir_JC4778 pectinesterase (EC 3.1.1.11) 1 - Arabidopsis thaliana >gi_550306_emb_CAA57275_(X81585) ATPME1 [Arabidopsis thaliana] >gi_903895_(U25649) ATPME1 precursor [Arabidopsis thaliana]

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Seq. No. 28956
Contig ID 183684_1.R1040
5'-most EST jC-gmle01810062d09a1

Seq. No. 28957
Contig ID 183714_1.R1040
5'-most EST jC-gmf102220070d06a1

Seq. No. 28958
Contig ID 183842_1.R1040
5'-most EST fde700875315.h1

Seq. No. 28959
Contig ID 183845_1.R1040
5'-most EST fde700875318.h1
Method BLASTX
NCBI GI g2947063
BLAST score 231
E value 4.0e-19
Match length 144
% identity 38
NCBI Description (AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No. 28960
Contig ID 183856_1.R1040
5'-most EST fde700875338.h1

Seq. No. 28961
Contig ID 183890_1.R1040
5'-most EST fde700875379.h1

Seq. No. 28962
Contig ID 183919_1.R1040
5'-most EST kl1701205968.h1

Seq. No. 28963
Contig ID 183975_1.R1040
5'-most EST fde700875494.h1
Method BLASTX
NCBI GI g1653767
BLAST score 330
E value 7.0e-31
Match length 121
% identity 53
NCBI Description (D90916) oligopeptidase A [Synechocystis sp.]

Seq. No. 28964
Contig ID 183992_1.R1040
5'-most EST g5677624

Seq. No. 28965
Contig ID 184065_1.R1040
5'-most EST fde700875620.h1

Seq. No. 28966
Contig ID 184078_1.R1040

[illegible]

Seq. No.	28968
Contig ID	184089_1.R1040
5'-most EST	jC-qmro02910012g06d1

Method	BLASTX
NCBI GI	g2244936
BLAST score	142
E value	5.0e-09

```
Seq. No.      28970
Contig ID     184119_1.R1040
5'-most EST   jC-qmle01810014e03d1
```

Method	BLASTX
NCBI GI	g2160173
BLAST score	263
E value	3.0e-23

Seq. No.	28972
Contig ID	184150_1.R1040
5'-most EST	pxt700941132.h1

Seq. No.	28974
Contig ID	184165_1.R1040
5'-most EST	fde700875776.h1

4472

Match length	73
% identity	56
NCBI Description	(U93215) regulatory protein Viviparous-1 isolog [Arabidopsis thaliana]
Seq. No.	28976
Contig ID	184206_1.R1040
5'-most EST	fde700875834.h1
Method	BLASTX
NCBI GI	g2245115
BLAST score	352
E value	3.0e-33
Match length	113
% identity	64
NCBI Description	(Z97343) unnamed protein product [Arabidopsis thaliana]
Seq. No.	28977
Contig ID	184207_1.R1040
5'-most EST	fde700875836.h1
Seq. No.	28978
Contig ID	184272_1.R1040
5'-most EST	jC-gmle01810080g05d1
Method	BLASTX
NCBI GI	g3242704
BLAST score	406
E value	2.0e-39
Match length	134
% identity	56
NCBI Description	(AC003040) hypothetical protein [Arabidopsis thaliana]
Seq. No.	28979
Contig ID	184280_1.R1040
5'-most EST	zsg701118495.h1
Seq. No.	28980
Contig ID	184304_1.R1040
5'-most EST	fde700875979.h1
Seq. No.	28981
Contig ID	184347_1.R1040
5'-most EST	fde700876044.h1
Seq. No.	28982
Contig ID	184382_1.R1040
5'-most EST	hrw701058203.h1
Seq. No.	28983
Contig ID	184402_1.R1040
5'-most EST	g5509131
Method	BLASTX
NCBI GI	g401213
BLAST score	352
E value	3.0e-33
Match length	118
% identity	58
NCBI Description	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE PRECURSOR >gi 166792

0968407-101000

BLAST score	150
E value	5.0e-10
Match length	78
% identity	36
NCBI Description	(D90906) 2-hydroxy-6-oxohepta-2,4-dienoate hydrolase [Synechocystis sp.]
Seq. No.	28993
Contig ID	184528_1.R1040
5'-most EST	jC-gmle01810040d01a1
Method	BLASTX
NCBI GI	g4455278
BLAST score	115
E value	2.0e-13
Match length	156
% identity	25
NCBI Description	(AL035527) hypothetical protein [Arabidopsis thaliana]
Seq. No.	28994
Contig ID	184530_1.R1040
5'-most EST	fde700877123.h1
Seq. No.	28995
Contig ID	184545_1.R1040
5'-most EST	fde700876343.h1
Seq. No.	28996
Contig ID	184597_1.R1040
5'-most EST	fde700876433.h1
Seq. No.	28997
Contig ID	184604_1.R1040
5'-most EST	fde700876445.h1
Method	BLASTX
NCBI GI	g1279911
BLAST score	441
E value	3.0e-44
Match length	84
% identity	98
NCBI Description	(U52963) mitogen-activated protein kinase [Nectria haematococca var. brevicona]
Seq. No.	28998
Contig ID	184612_1.R1040
5'-most EST	fde700876454.h1
Method	BLASTX
NCBI GI	g3522948
BLAST score	357
E value	8.0e-34
Match length	143
% identity	54
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]
Seq. No.	28999
Contig ID	184628_1.R1040
5'-most EST	g5342489
Method	BLASTX

NCBI Description (279754) similar to nucleoside diphosphate kinase; cDNA EST CEMSG50F comes from this gene; cDNA EST EMBL:D71761 comes from this gene; cDNA EST EMBL:D72901 comes from this gene; cDNA EST EMBL:D72956 comes from this gene; cDNA ES

Seq. No. 29005
Contig ID 184713_1.R1040
5'-most EST fde700876604.h1

Seq. No. 29006
Contig ID 184749_1.R1040
5'-most EST sat701012630.h1
Method BLASTX
NCBI GI g2160692
BLAST score 863
E value 4.0e-93
Match length 193
% identity 83

NCBI Description (U73527) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No. 29007
Contig ID 184792_1.R1040
5'-most EST fde700876732.h1
Method BLASTX
NCBI GI g3025189
BLAST score 178
E value 3.0e-13
Match length 69
% identity 57

NCBI Description HYPOTHETICAL 67.1 KD PROTEIN SLL1770
>gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis sp.]

Seq. No. 29008
Contig ID 184804_1.R1040
5'-most EST zsg701119021.h1
Method BLASTX
NCBI GI g2344854
BLAST score 161
E value 1.0e-10
Match length 128
% identity 36

NCBI Description (Z98756) endopeptidase IV [Mycobacterium leprae]

Seq. No. 29009
Contig ID 184808_1.R1040
5'-most EST zsg701118427.h1
Method BLASTX
NCBI GI g2842482
BLAST score 183
E value 1.0e-13
Match length 73
% identity 41

NCBI Description (AL021749) protein phosphatase 2C-like protein [Arabidopsis thaliana]


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Seq. No.          29010
Contig ID         184816_1.R1040
5'-most EST      zhf700955674.h1
Method            BLASTX
NCBI GI           g2262116
BLAST score       247
E value           4.0e-21
Match length      122
% identity        43
NCBI Description  (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
```

Seq. No.	29011
Contig ID	184840_1.R1040
5'-most EST	jex700909913.h1

Seq. No.	29012
Contig ID	184850_1.R1040
5'-most EST	fde700877149.h1

```
Seq. No.          29013
Contig ID         184856_1.R1040
5'-most EST      fde700876844.h1
Method            BLASTX
NCBI GI           g1076334
BLAST score       175
E value           6.0e-13
Match length      82
% identity        48
NCBI Description  hypothetical protein HYP1 - Arabidopsis thaliana
                  >gi_499168_emb_CAA56145_ (X79707) HYP1 [Arabidopsis
                  thaliana]
```

```
Seq. No.      29014
Contig ID     184860_1.R1040
5'-most EST   fua701041059.h1
```

Seq. No.	29015
Contig ID	184869_1.R1040
5'-most EST	fde700876880.h1

Seq. No.	29016
Contig ID	184876_1.R1040
5'-most EST	sat701011851.h1

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Seq. No.          29017
Contig ID         184877_1.R1040
5'-most EST      dpv701102090.h1
Method            BLASTX
NCBI GI           g3355477
BLAST score       425
E value           3.0e-42
Match length      91
% identity        50
NCBI Description  (AC004218) putative P-glycoprotein, pgp1 [Arabidopsis
                  thaliana]
```

Seq. No. 29018

Seq. No. 29025
 Contig ID 185098_1.R1040
 5'-most EST hrw701057980.h1
 Method BLASTX
 NCBI GI g2880047
 BLAST score 481
 E value 2.0e-48
 Match length 132
 % identity 70
 NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29026
 Contig ID 185110_1.R1040
 5'-most EST jC-gmle01810024e05a1
 Method BLASTX
 NCBI GI g3928543
 BLAST score 196
 E value 8.0e-15
 Match length 139
 % identity 35
 NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No. 29027
 Contig ID 185147_1.R1040
 5'-most EST fde700877282.h1
 Method BLASTX
 NCBI GI g3341693
 BLAST score 163
 E value 2.0e-11
 Match length 74
 % identity 45
 NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 29028
 Contig ID 185191_1.R1040
 5'-most EST leu701156146.h1

Seq. No. 29029
 Contig ID 185202_2.R1040
 5'-most EST gsv701047468.h1
 Method BLASTX
 NCBI GI g3024871
 BLAST score 357
 E value 4.0e-34
 Match length 111
 % identity 57
 NCBI Description HYPOTHETICAL 77.3 KD PROTEIN SLL0005
 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No. 29030
 Contig ID 185205_1.R1040
 5'-most EST xzm700763756.h1
 Method BLASTX
 NCBI GI g1707642
 BLAST score 348

Match length	146
% identity	63
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]
Seq. No.	29049
Contig ID	185480_1.R1040
5'-most EST	asn701139454.h1
Seq. No.	29050
Contig ID	185483_1.R1040
5'-most EST	zhf700963571.h1
Seq. No.	29051
Contig ID	185486_1.R1040
5'-most EST	zzp700829606.h1
Method	BLASTX
NCBI GI	g2493318
BLAST score	265
E value	2.0e-23
Match length	76
% identity	74
NCBI Description	BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_ (Z25471) blue copper protein [Pisum sativum] >gi_1098264_prf_2115352A blue Cu protein [Pisum sativum]
Seq. No.	29052
Contig ID	185527_1.R1040
5'-most EST	jex700905589.h1
Seq. No.	29053
Contig ID	185547_1.R1040
5'-most EST	zzp700832556.h1
Method	BLASTX
NCBI GI	g1076715
BLAST score	172
E value	1.0e-12
Match length	57
% identity	53
NCBI Description	abscisic acid-induced protein HVA22 - barley >gi_404589 (L19119) A22 [Hordeum vulgare]
Seq. No.	29054
Contig ID	185557_1.R1040
5'-most EST	jex700903613.h1
Method	BLASTX
NCBI GI	g1710663
BLAST score	392
E value	2.0e-38
Match length	90
% identity	77
NCBI Description	PUTATIVE DNA-DIRECTED RNA POLYMERASE III 130 KD POLYPEPTIDE (RNA POLYMERASE III SUBUNIT 2) >gi_1204209_emb_CAA93558 (Z69727) putative DNA-directed RNA polymerase III 130 kd subunit [Schizosaccharomyces pombe]
Seq. No.	29055

Seq. No. 29064
 Contig ID 185679_1.R1040
 5'-most EST jsh701070177.h1
 Method BLASTX
 NCBI GI g349379
 BLAST score 404
 E value 8.0e-40
 Match length 87
 % identity 91
 NCBI Description (L22847) HAHB-1 [*Helianthus annuus*]

Seq. No. 29065
 Contig ID 185683_1.R1040
 5'-most EST sat701009239.h1

Seq. No. 29066
 Contig ID 185684_1.R1040
 5'-most EST asn701132976.h1

Seq. No. 29067
 Contig ID 185694_1.R1040
 5'-most EST zzp700830049.h1
 Method BLASTX
 NCBI GI g3688177
 BLAST score 479
 E value 6.0e-48
 Match length 128
 % identity 70
 NCBI Description (AL031804) putative protein [*Arabidopsis thaliana*]

Seq. No. 29068
 Contig ID 185754_1.R1040
 5'-most EST zzp700830288.h1
 Method BLASTX
 NCBI GI g4097522
 BLAST score 586
 E value 2.0e-60
 Match length 142
 % identity 80
 NCBI Description (U63534) cinnamyl alcohol dehydrogenase [*Fragaria x ananassa*]

Seq. No. 29069
 Contig ID 185765_1.R1040
 5'-most EST zzp700830201.h1

Seq. No. 29070
 Contig ID 185786_1.R1040
 5'-most EST jC-gmro02910052f11a1

Seq. No. 29071
 Contig ID 185800_1.R1040
 5'-most EST jC-gmst02400044h01a1

Seq. No. 29072
 Contig ID 185812_1.R1040
 5'-most EST zzp700830276.h1

00000000000000000000000000000000

Seq. No.	29081
Contig ID	185983_1.R1040
5'-most EST	fua701039571.h1

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Seq. No.      29083
Contig ID     185994_2.R1040
5'-most EST   zzp700830606.h1
```

```
Seq. No.          29084
Contig ID         186007_1.R1040
5'-most EST      uC-gmrominsoy246d04b1
Method            BLASTX
NCBI GI           g3135273
BLAST score       308
E value           4.0e-28
Match length      120
% identity        53
NCBI Description  (AC003058) hypothetical protein [Arabidopsis thaliana]
                  >gi_4191773 (AC005917) putative WD-40 repeat protein
                  [Arabidopsis thaliana]
```

```
Seq. No.          29085
Contig ID         186011_1.R1040
5'-most EST      uC-gmropic102h03b1
Method            BLASTX
NCBI GI           g3319349
BLAST score       246
E value           6.0e-21
Match length      119
% identity        43
NCBI Description  (AF077407) No definition line found [Arabidopsis thaliana]
```

Seq. No.	29086
Contig ID	186029_1.R1040
5'-most EST	zzp700830656.h1

Seq. No.	29087
Contig ID	186035_1.R1040
5'-most EST	zzp700830663.h1

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 29118
 Contig ID 186518_1.R1040
 5'-most EST zzp700831430.h1
 Method BLASTN
 NCBI GI g4159704
 BLAST score 35
 E value 6.0e-10
 Match length 71
 % identity 87
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
 MCB17, complete sequence [Arabidopsis thaliana]

Seq. No. 29119
 Contig ID 186539_1.R1040
 5'-most EST zzp700831477.h1

Seq. No. 29120
 Contig ID 186548_1.R1040
 5'-most EST zzp700831491.h1
 Method BLASTX
 NCBI GI g3947735
 BLAST score 379
 E value 2.0e-36
 Match length 119
 % identity 61
 NCBI Description (AJ009720) NL27 [Solanum tuberosum]

Seq. No. 29121
 Contig ID 186556_1.R1040
 5'-most EST hrw701060646.h1
 Method BLASTX
 NCBI GI g2252631
 BLAST score 312
 E value 1.0e-28
 Match length 115
 % identity 61
 NCBI Description (U95973) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29122
 Contig ID 186574_1.R1040
 5'-most EST zzp700831529.h1
 Method BLASTX
 NCBI GI g4539321
 BLAST score 271
 E value 8.0e-24
 Match length 69
 % identity 70
 NCBI Description (AL035679) putative protein [Arabidopsis thaliana]

Seq. No. 29123
 Contig ID 186584_1.R1040
 5'-most EST zzp700831550.h1

Seq. No. 29124
 Contig ID 186656_1.R1040

5'-most EST uC-gmropic101e02b1
 Method BLASTX
 NCBI GI g4510401
 BLAST score 371
 E value 1.0e-35
 Match length 85
 % identity 72
 NCBI Description (AC006587) putative general negative regulator of transcription [Arabidopsis thaliana]

Seq. No. 29125
 Contig ID 186658_1.R1040
 5'-most EST jC-gmst02400033f02a1
 Method BLASTX
 NCBI GI g2529677
 BLAST score 216
 E value 2.0e-17
 Match length 120
 % identity 42
 NCBI Description (AC002535) kinesin-like protein, heavy chain [Arabidopsis thaliana]

Seq. No. 29126
 Contig ID 186662_1.R1040
 5'-most EST uC-gmromins083d10b1

Seq. No. 29127
 Contig ID 186662_2.R1040
 5'-most EST leu701147412.h1

Seq. No. 29128
 Contig ID 186677_1.R1040
 5'-most EST gsv701049260.h1

Seq. No. 29129
 Contig ID 186697_1.R1040
 5'-most EST zzp700831730.h1

Seq. No. 29130
 Contig ID 186734_1.R1040
 5'-most EST kl1701202390.h1

Seq. No. 29131
 Contig ID 186756_1.R1040
 5'-most EST zzp700831811.h1

Seq. No. 29132
 Contig ID 186789_1.R1040
 5'-most EST zzp700831860.h1
 Method BLASTN
 NCBI GI g2828183
 BLAST score 46
 E value 8.0e-17
 Match length 82
 % identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No. 29164
Contig ID 187355_1.R1040
5'-most EST dpv701103408.h1

Seq. No. 29165
Contig ID 187392_1.R1040
5'-most EST zhf700953442.h1

Seq. No. 29166
Contig ID 187411_1.R1040
5'-most EST pmv700892727.h1

Seq. No. 29167
Contig ID 187468_1.R1040
5'-most EST g4290412

Seq. No. 29168
Contig ID 187485_1.R1040
5'-most EST zzp700832828.h1

Seq. No. 29169
Contig ID 187501_1.R1040
5'-most EST jC-gmro02910061d07a1

Seq. No. 29170
Contig ID 187515_1.R1040
5'-most EST zzp700832864.h1
Method BLASTX
NCBI GI g3021270
BLAST score 371
E value 2.0e-35
Match length 122
% identity 59
NCBI Description (AL022347) serine/threonine kinase -like protein
[Arabidopsis thaliana]

Seq. No. 29171
Contig ID 187527_1.R1040
5'-most EST zzp700832881.h1
Method BLASTX
NCBI GI g3608495
BLAST score 339
E value 4.0e-32
Match length 82
% identity 82
NCBI Description (AF089738) plastid division protein FtsZ [Arabidopsis thaliana] >gi_4510351_gb_AAD21440.1_ (AC006921) plastid division protein FtsZ [Arabidopsis thaliana]

Seq. No. 29172
Contig ID 187535_1.R1040
5'-most EST zzp700832890.h1
Method BLASTX
NCBI GI g3335341
BLAST score 204
E value 3.0e-16
Match length 84

09684016.101000

```
% identity      55
NCBI Description (AC004512) T8F5.10 [Arabidopsis thaliana]

Seq. No.        29173
Contig ID       187537_1.R1040
5'-most EST     asn701135218.h1

Seq. No.        29174
Contig ID       187547_1.R1040
5'-most EST     uC-gmrominsoy171e09b1

Seq. No.        29175
Contig ID       187594_1.R1040
5'-most EST     zzp700833073.h1

Seq. No.        29176
Contig ID       187598_1.R1040
5'-most EST     uC-gmrominsoy117g12b1
Method          BLASTX
NCBI GI         g4337174
BLAST score     246
E value         5.0e-21
Match length    117
% identity      50
NCBI Description (AC006416) Similar to gi_1573829 HI0816 aminopeptidase P
homolog (pepP) from Haemophilus influenzae genome
gb_U32764. [Arabidopsis thaliana]

Seq. No.        29177
Contig ID       187602_1.R1040
5'-most EST     fua701037621.h1

Seq. No.        29178
Contig ID       187621_1.R1040
5'-most EST     uC-gmropic004a03b1

Seq. No.        29179
Contig ID       187622_1.R1040
5'-most EST     zzp700833005.h1

Seq. No.        29180
Contig ID       187631_1.R1040
5'-most EST     sat701014046.h1

Seq. No.        29181
Contig ID       187656_1.R1040
5'-most EST     zzp700833048.h1

Seq. No.        29182
Contig ID       187712_1.R1040
5'-most EST     hrw701058357.h1
Method          BLASTX
NCBI GI         g3236235
BLAST score     357
E value         3.0e-34
Match length    77
% identity      81
```


BLAST score 36
 E value 6.0e-11
 Match length 88
 % identity 85
 NCBI Description Arabidopsis thaliana chromosome II BAC T2G17 genomic
 sequence, complete sequence

Seq. No. 29190
 Contig ID 187853_1.R1040
 5'-most EST zhf700960325.h1
 Method BLASTX
 NCBI GI g3157942
 BLAST score 149
 E value 6.0e-10
 Match length 73
 % identity 49
 NCBI Description (AC002131) Similar to style development-specific protein
 9612 precursor gb_X55193 and pectate lyase P59 precursor
 gb_X15499 from Lycopersicon esculentum. [Arabidopsis
 thaliana]

Seq. No. 29191
 Contig ID 187858_1.R1040
 5'-most EST zzp700833309.h1

Seq. No. 29192
 Contig ID 187870_1.R1040
 5'-most EST zhf700952319.h1

Seq. No. 29193
 Contig ID 187870_2.R1040
 5'-most EST jex700908277.h1

Seq. No. 29194
 Contig ID 187878_1.R1040
 5'-most EST zzp700833333.h1

Seq. No. 29195
 Contig ID 187882_1.R1040
 5'-most EST zzp700833337.h1
 Method BLASTX
 NCBI GI g3608263
 BLAST score 322
 E value 6.0e-30
 Match length 82
 % identity 76
 NCBI Description (AB017565) Dof zinc finger protein [Arabidopsis thaliana]

Seq. No. 29196
 Contig ID 187898_1.R1040
 5'-most EST zzp700833362.h1

Seq. No. 29197
 Contig ID 187904_1.R1040
 5'-most EST zzp700833369.h1

Seq. No. 29198

09684015 101000

Contig ID 187917_1.R1040
5'-most EST zzp700833386.h1

Seq. No. 29199
Contig ID 187922_1.R1040
5'-most EST uC-gmropic101d01b1
Method BLASTX
NCBI GI g3063449
BLAST score 511
E value 7.0e-52
Match length 137
% identity 70
NCBI Description (AC003981) F22013.11 [Arabidopsis thaliana]

Seq. No. 29200
Contig ID 187929_1.R1040
5'-most EST sat701003791.h1

Seq. No. 29201
Contig ID 187955_1.R1040
5'-most EST zzp700836295.h1
Method BLASTN
NCBI GI g4432829
BLAST score 33
E value 4.0e-09
Match length 41
% identity 95
NCBI Description Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 29202
Contig ID 187970_1.R1040
5'-most EST zhf700954165.h1
Method BLASTX
NCBI GI g3128192
BLAST score 794
E value 5.0e-85
Match length 190
% identity 78
NCBI Description (AC004521) axi 1-like protein [Arabidopsis thaliana]

Seq. No. 29203
Contig ID 187997_1.R1040
5'-most EST uC-gmrominsoy224g06b1

Seq. No. 29204
Contig ID 188021_1.R1040
5'-most EST uC-gmropic089h09b1

Seq. No. 29205
Contig ID 188026_1.R1040
5'-most EST sat701008619.h1

Seq. No. 29206
Contig ID 188093_1.R1040
5'-most EST fC-gmse7000764839f1

Seq. No. 29207
 Contig ID 188105_1.R1040
 5'-most EST jC-gmst02400060e10d1

Seq. No. 29208
 Contig ID 188118_1.R1040
 5'-most EST zzp700833677.h1
 Method BLASTX
 NCBI GI g4567279
 BLAST score 353
 E value 3.0e-33
 Match length 142
 % identity 52
 NCBI Description (AC006841) putative serine/threonine protein kinase
 [Arabidopsis thaliana]

Seq. No. 29209
 Contig ID 188119_1.R1040
 5'-most EST gsv701053208.h1

Seq. No. 29210
 Contig ID 188126_1.R1040
 5'-most EST pxt700945449.h1

Seq. No. 29211
 Contig ID 188128_1.R1040
 5'-most EST gsv701048757.h1
 Method BLASTX
 NCBI GI g4538961
 BLAST score 937
 E value 1.0e-101
 Match length 205
 % identity 80
 NCBI Description (AL049488) isoleucine-tRNA ligase-like protein [Arabidopsis
 thaliana]

Seq. No. 29212
 Contig ID 188156_1.R1040
 5'-most EST bth700848590.h1
 Method BLASTX
 NCBI GI g4262224
 BLAST score 159
 E value 3.0e-14
 Match length 67
 % identity 64
 NCBI Description (AC006200) putative amino acid or GABA permease
 [Arabidopsis thaliana]

Seq. No. 29213
 Contig ID 188172_1.R1040
 5'-most EST zzp700833757.h1

Seq. No. 29214
 Contig ID 188183_1.R1040
 5'-most EST zzp700833768.h1

Seq. No. 29215

5'-most EST jex700907604.h1
 Method BLASTX
 NCBI GI g3881761
 BLAST score 158
 E value 2.0e-10
 Match length 123
 % identity 35
 NCBI Description (Z37093) alternative splicing in ZK669.1a; cDNA EST
 EMBL:D36754 comes from this gene [Caenorhabditis elegans]
 >gi_3881779_emb_CAA86848 (Z46812) alternative splicing in
 ZK669.1a; cDNA EST EMBL:D36754 comes from this gene
 [Caenorhabditis elegans]

Seq. No. 29236
 Contig ID 188447_1.R1040
 5'-most EST fC-gmse700646582g1

Seq. No. 29237
 Contig ID 188469_1.R1040
 5'-most EST gsv701056189.h1

Seq. No. 29238
 Contig ID 188509_1.R1040
 5'-most EST zzp700834153.h1

Seq. No. 29239
 Contig ID 188517_1.R1040
 5'-most EST uC-gmrominsoy035f10b1

Seq. No. 29240
 Contig ID 188542_1.R1040
 5'-most EST zhf700954428.h1
 Method BLASTX
 NCBI GI g4510339
 BLAST score 251
 E value 1.0e-21
 Match length 75
 % identity 44
 NCBI Description (AC006921) putative ABC transporter protein [Arabidopsis
 thaliana]

Seq. No. 29241
 Contig ID 188548_1.R1040
 5'-most EST pxt700946279.h1

Seq. No. 29242
 Contig ID 188568_1.R1040
 5'-most EST uC-gmflminsoy075h06b1
 Method BLASTX
 NCBI GI g2224695
 BLAST score 552
 E value 9.0e-57
 Match length 150
 % identity 68
 NCBI Description (AB002375) KIAA0377 [Homo sapiens]

Seq. No. 29243

Seq. No.	29271
Contig ID	189024_1.R1040
5'-most EST	zzp700834874.h1
Method	BLASTX
NCBI GI	g4567279
BLAST score	455
E value	2.0e-45
Match length	140
% identity	63
NCBI Description	(AC006841) putative serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	29272
Contig ID	189062_1.R1040
5'-most EST	jC-gmfl02220064g02a1
Seq. No.	29273
Contig ID	189077_1.R1040
5'-most EST	zzp700834944.h1
Seq. No.	29274
Contig ID	189082_1.R1040
5'-most EST	zzp700834949.h1
Method	BLASTX
NCBI GI	g119640
BLAST score	163
E value	2.0e-11
Match length	74
% identity	42
NCBI Description	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN E8) >gi_82109_pir_S01642 ripening protein E8 - tomato >gi_19199_emb_CAA31789_ (X13437) E8 protein [Lycopersicon esculentum]
Seq. No.	29275
Contig ID	189091_1.R1040
5'-most EST	jC-gmst02400055c07a1
Seq. No.	29276
Contig ID	189100_1.R1040
5'-most EST	uC-gmröpic022b04b1
Method	BLASTX
NCBI GI	g1854443
BLAST score	585
E value	2.0e-60
Match length	132
% identity	83
NCBI Description	(D83970) CPRD8 protein [Vigna unguiculata]
Seq. No.	29277
Contig ID	189103_1.R1040
5'-most EST	zzp700834976.h1
Seq. No.	29278
Contig ID	189120_1.R1040
5'-most EST	jC-gmle01810012a03a1

Seq. No.	29279
Contig ID	189126_1.R1040
5'-most EST	jC-gmle01810004e12d1
Method	BLASTX
NCBI GI	g4538987
BLAST score	182
E value	2.0e-13
Match length	47
% identity	68
NCBI Description	(AJ133777) gamma-adaptin 2 [Arabidopsis thaliana]
Seq. No.	29280
Contig ID	189173_1.R1040
5'-most EST	kl1701206401.h1
Seq. No.	29281
Contig ID	189202_1.R1040
5'-most EST	g4397430
Seq. No.	29282
Contig ID	189207_1.R1040
5'-most EST	zzp700835112.h1
Seq. No.	29283
Contig ID	189235_1.R1040
5'-most EST	zzp700835146.h1
Seq. No.	29284
Contig ID	189248_1.R1040
5'-most EST	zzp700835167.h1
Method	BLASTX
NCBI GI	g3402704
BLAST score	177
E value	8.0e-13
Match length	83
% identity	41
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]
Seq. No.	29285
Contig ID	189279_1.R1040
5'-most EST	g4292541
Method	BLASTX
NCBI GI	g559237
BLAST score	351
E value	2.0e-33
Match length	110
% identity	65
NCBI Description	(L36982) tyrosine-rich hydroxyproline-rich glycoprotein [Petroselinum crispum]
Seq. No.	29286
Contig ID	189286_1.R1040
5'-most EST	zzp700835214.h1
Method	BLASTX
NCBI GI	g1170626
BLAST score	448

E value 8.0e-45
 Match length 103
 % identity 84
 NCBI Description CALCIUM/CALMODULIN-DEPENDENT SERINE/THREONINE PROTEIN KINASE >gi_478408_pir_JQ2251 calcium/calmodulin-binding protein kinase - apple tree >gi_311320_emb_CAA78961_(Z17313) calcium/calmodulin-dependent serine/threonine protein kinase [Malus domestica] >gi_984160_emb_CAA86286_(Z38126) calmodulin-binding protein kinase [Malus domestica]

Seq. No. 29287
 Contig ID 189295_1.R1040
 5'-most EST zzp700835225.h1
 Method BLASTX
 NCBI GI g4432860
 BLAST score 166
 E value 3.0e-11
 Match length 120
 % identity 8
 NCBI Description (AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No. 29288
 Contig ID 189325_1.R1040
 5'-most EST zzp700835263.h1

Seq. No. 29289
 Contig ID 189344_1.R1040
 5'-most EST zzp700835285.h1

Seq. No. 29290
 Contig ID 189349_1.R1040
 5'-most EST uC-gmropic074c08b1

Seq. No. 29291
 Contig ID 189375_1.R1040
 5'-most EST zzp700835330.h1

Seq. No. 29292
 Contig ID 189382_1.R1040
 5'-most EST dpv701098653.h1

Seq. No. 29293
 Contig ID 189395_1.R1040
 5'-most EST jC-gmle01810069h03d1

Seq. No. 29294
 Contig ID 189399_1.R1040
 5'-most EST zzp700835359.h1
 Method BLASTX
 NCBI GI g2829912
 BLAST score 308
 E value 2.0e-28
 Match length 72
 % identity 82
 NCBI Description (AC002291) Similar ATP-dependent RNA Helicase [Arabidopsis

[illegible]

```
Seq. No.          29296
Contig ID         189432_1.R1040
5'-most EST      jC-gmst02400071a12a1
Method            BLASTX
NCBI GI           g3641845
BLAST score       172
E value           4.0e-12
Match length      74
% identity        49
NCBI Description  (AJ223358) stelar K+ outward rectifying channel
                  [Arabidopsis thaliana]
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Seq. No.          29298
Contig ID         189481_1.R1040
5'-most EST      zzp700835461.h1
Method            BLASTX
NCBI GI           g2335096
BLAST score       164
E value           8.0e-12
Match length      55
% identity        62
NCBI Description  (AC002339) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.          29300
Contig ID         189532_1.R1040
5'-most EST      dpv701101315.h1
Method            BLASTX
NCBI GI           g3023519
BLAST score       210
E value           7.0e-29
Match length      113
% identity        58
NCBI Description  ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT
                  (ENDOPEPTIDASE CLP) >gi_2384690 (AF013216) proteosome major
                  subunit [Myxococcus xanthus]
```


Seq. No.	29301
Contig ID	189548_1.R1040
5'-most EST	uC-gmropic022a06b1
Seq. No.	29302
Contig ID	189557_1.R1040
5'-most EST	g5175508
Seq. No.	29303
Contig ID	189565_1.R1040
5'-most EST	jC-gmle01810005b06a1
Seq. No.	29304
Contig ID	189575_1.R1040
5'-most EST	jC-gmle01810080a08d1
Seq. No.	29305
Contig ID	189589_1.R1040
5'-most EST	dpr701103654.h1
Seq. No.	29306
Contig ID	189638_1.R1040
5'-most EST	zzp700835668.h1
Seq. No.	29307
Contig ID	189641_1.R1040
5'-most EST	uC-gmrominsoy219d04b1
Seq. No.	29308
Contig ID	189643_1.R1040
5'-most EST	zzp700835673.h1
Seq. No.	29309
Contig ID	189650_1.R1040
5'-most EST	uC-gmropic056e01b1
Seq. No.	29310
Contig ID	189653_1.R1040
5'-most EST	jC-gmst02400031c10a1
Method	BLASTX
NCBI GI	g4567304
BLAST score	583
E value	6.0e-60
Match length	238
% identity	53
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]
Seq. No.	29311
Contig ID	189670_1.R1040
5'-most EST	zzp700835712.h1
Seq. No.	29312
Contig ID	189678_1.R1040
5'-most EST	jC-gmle01810010g04a1
Seq. No.	29313
Contig ID	189725_1.R1040

000101" 9104350

Contig ID 190037_1.R1040
 5'-most EST crh700855395.h1
 Method BLASTX
 NCBI GI g2688822
 BLAST score 518
 E value 2.0e-52
 Match length 132
 % identity 73
 NCBI Description (U93272) pyrophosphate-dependent phosphofructo-1-kinase
 [Prunus armeniaca]

Seq. No. 29328
 Contig ID 190066_1.R1040
 5'-most EST zzp700836223.h1
 Method BLASTX
 NCBI GI g4056403
 BLAST score 191
 E value 9.0e-15
 Match length 72
 % identity 62
 NCBI Description (AD001673) lipoxygenase [Persea americana]

Seq. No. 29329
 Contig ID 190069_1.R1040
 5'-most EST zzp700836236.h1
 Method BLASTX
 NCBI GI g3402675
 BLAST score 248
 E value 8.0e-21
 Match length 137
 % identity 40
 NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29330
 Contig ID 190078_1.R1040
 5'-most EST zzp700836239.h1

Seq. No. 29331
 Contig ID 190081_1.R1040
 5'-most EST zzp700836243.h1

Seq. No. 29332
 Contig ID 190088_1.R1040
 5'-most EST uC-gmrominsoy028d10b1

Seq. No. 29333
 Contig ID 190214_1.R1040
 5'-most EST uC-gmrominsoy099e05b1

Seq. No. 29334
 Contig ID 190220_1.R1040
 5'-most EST sat701002720.h2
 Method BLASTX
 NCBI GI g3819699
 BLAST score 431
 E value 2.0e-42
 Match length 119

5'-most EST sat701003065.h1
Seq. No. 29350
Contig ID 190516_1.R1040
5'-most EST sat701003104.h1

Seq. No. 29351
Contig ID 190522_1.R1040
5'-most EST sat701003112.h1
Method BLASTN
NCBI GI g1619601
BLAST score 112
E value 3.0e-56
Match length 188
% identity 90
NCBI Description M.truncatula mRNA for MtN3 gene

Seq. No. 29352
Contig ID 190526_1.R1040
5'-most EST jC-gmst02400063h04a1

Seq. No. 29353
Contig ID 190534_1.R1040
5'-most EST sat701003129.h1
Method BLASTX
NCBI GI g4455232
BLAST score 167
E value 2.0e-11
Match length 164
% identity 34
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 29354
Contig ID 190556_1.R1040
5'-most EST sat701003164.h1
Method BLASTN
NCBI GI g2224910
BLAST score 58
E value 5.0e-24
Match length 170
% identity 84
NCBI Description Daucus carota somatic embryogenesis receptor-like kinase mRNA, complete cds

Seq. No. 29355
Contig ID 190592_1.R1040
5'-most EST sat701003209.h1

Seq. No. 29356
Contig ID 190599_1.R1040
5'-most EST pmv700894036.h1
Method BLASTX
NCBI GI g3834306
BLAST score 165
E value 2.0e-11
Match length 90
% identity 42

Seq. No. 29381
 Contig ID 191020_1.R1040
 5'-most EST uC-gmflminsoy074g01b1
 Method BLASTX
 NCBI GI g4056496
 BLAST score 263
 E value 6.0e-23
 Match length 68
 % identity 76
 NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 29382
 Contig ID 191043_1.R1040
 5'-most EST k11701202887.h1

Seq. No. 29383
 Contig ID 191054_1.R1040
 5'-most EST sat701003880.h1

Seq. No. 29384
 Contig ID 191063_1.R1040
 5'-most EST g5175467
 Method BLASTX
 NCBI GI g3080401
 BLAST score 480
 E value 5.0e-48
 Match length 140
 % identity 64
 NCBI Description (AL022603) putative protein [Arabidopsis thaliana]
 >gi_4455265_emb_CAB36801.1_ (AL035527) putative protein
 [Arabidopsis thaliana]

Seq. No. 29385
 Contig ID 191143_1.R1040
 5'-most EST sat701004031.h1

Seq. No. 29386
 Contig ID 191147_1.R1040
 5'-most EST pxt700944436.h1
 Method BLASTX
 NCBI GI g1841464
 BLAST score 390
 E value 1.0e-37
 Match length 109
 % identity 39
 NCBI Description (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No. 29387
 Contig ID 191153_1.R1040
 5'-most EST sat701004047.h1

Seq. No. 29388
 Contig ID 191172_1.R1040
 5'-most EST jC-gmlē01810020g12a1
 Method BLASTX
 NCBI GI g2335096

NCBI GI g1076274
 BLAST score 333
 E value 3.0e-31
 Match length 121
 % identity 59
 NCBI Description cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)

Seq. No. 29409
 Contig ID 191605_1.R1040
 5'-most EST uC-gmrominsoy224a09b1
 Method BLASTX
 NCBI GI g2224933
 BLAST score 171
 E value 5.0e-12
 Match length 56
 % identity 61
 NCBI Description (AF004216) ethylene-insensitive3 [Arabidopsis thaliana]
 >gi_2224935 (AF004217) ethylene-insensitive3 [Arabidopsis thaliana]

Seq. No. 29410
 Contig ID 191625_1.R1040
 5'-most EST sat701004679.h1
 Method BLASTX
 NCBI GI g2129859
 BLAST score 534
 E value 1.0e-54
 Match length 141
 % identity 69
 NCBI Description vestitone reductase - alfalfa >gi_973249 (U28213) vestitone reductase [Medicago sativa subsp. sativa]

Seq. No. 29411
 Contig ID 191633_1.R1040
 5'-most EST sat701004688.h1

Seq. No. 29412
 Contig ID 191646_1.R1040
 5'-most EST jC-gmle01810061h01a1

Seq. No. 29413
 Contig ID 191655_1.R1040
 5'-most EST fua701037394.h1
 Method BLASTX
 NCBI GI g3668085
 BLAST score 171
 E value 1.0e-11
 Match length 124
 % identity 52
 NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29414
 Contig ID 191655_2.R1040
 5'-most EST gsv701044364.h1
 Method BLASTX
 NCBI GI g3668085
 BLAST score 151

000101 91048960

E value 1.0e-09
Match length 95
% identity 41
NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29415
Contig ID 191659_1.R1040
5'-most EST sat701009643.h1
Method BLASTX
NCBI GI g4538934
BLAST score 288
E value 3.0e-26
Match length 91
% identity 37
NCBI Description (AL049483) putative leucine-rich-repeat protein [Arabidopsis thaliana]

Seq. No. 29416
Contig ID 191700_1.R1040
5'-most EST sat701004787.h1

Seq. No. 29417
Contig ID 191737_1.R1040
5'-most EST gsv701051086.h1

Seq. No. 29418
Contig ID 191779_1.R1040
5'-most EST jC-gmf102220138g07a1
Method BLASTX
NCBI GI g1076664
BLAST score 356
E value 9.0e-34
Match length 150
% identity 53
NCBI Description leucine zipper transcription factor - potato
>gi_575418_emb_CAA57894_(X82544) leucine zipper
transcription factor [Solanum tuberosum]

Seq. No. 29419
Contig ID 191811_1.R1040
5'-most EST sat701004943.h1
Method BLASTX
NCBI GI g3426039
BLAST score 234
E value 2.0e-19
Match length 101
% identity 50
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 29420
Contig ID 191825_1.R1040
5'-most EST jC-gmro02910023e02d1
Method BLASTX
NCBI GI g2827992
BLAST score 587
E value 7.0e-61
Match length 145

Contig ID 192694_1.R1040
 5'-most EST uC-gmrominsoy217b04b1
 Method BLASTX
 NCBI GI g2292921
 BLAST score 419
 E value 2.0e-52
 Match length 152
 % identity 73
 NCBI Description (Y10252) pantoate--beta-alanine ligase [Lotus japonicus]

Seq. No. 29475
 Contig ID 192722_1.R1040
 5'-most EST uC-gmropic032c09b1
 Method BLASTX
 NCBI GI g4530585
 BLAST score 208
 E value 2.0e-16
 Match length 51
 % identity 71
 NCBI Description (AF130978) B12D protein [Ipomoea batatas]

Seq. No. 29476
 Contig ID 192722_2.R1040
 5'-most EST sat701006550.h1
 Method BLASTX
 NCBI GI g4530585
 BLAST score 354
 E value 2.0e-33
 Match length 87
 % identity 70
 NCBI Description (AF130978) B12D protein [Ipomoea batatas]

Seq. No. 29477
 Contig ID 192730_1.R1040
 5'-most EST zsg701128511.h1
 Method BLASTX
 NCBI GI g3201627
 BLAST score 363
 E value 2.0e-40
 Match length 114
 % identity 68
 NCBI Description (AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No. 29478
 Contig ID 192760_1.R1040
 5'-most EST sat701006609.h1
 Method BLASTX
 NCBI GI g3688173
 BLAST score 454
 E value 3.0e-45
 Match length 134
 % identity 60
 NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 29479
 Contig ID 192777_1.R1040
 5'-most EST sat701006632.h1

5'-most EST	sat701007370.h2
Seq. No.	29498
Contig ID	193153_1.R1040
5'-most EST	sat701007377.h2
Seq. No.	29499
Contig ID	193161_1.R1040
5'-most EST	uC-gmropic069h12b1
Seq. No.	29500
Contig ID	193166_1.R1040
5'-most EST	jC-gmst02400029f06a1
Seq. No.	29501
Contig ID	193180_1.R1040
5'-most EST	kl1701207080.h1
Seq. No.	29502
Contig ID	193209_1.R1040
5'-most EST	g4314091
Method	BLASTX
NCBI GI	g3822223
BLAST score	1022
E value	1.0e-111
Match length	255
% identity	73
NCBI Description	(AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]
Seq. No.	29503
Contig ID	193214_1.R1040
5'-most EST	sat701007463.h2
Method	BLASTX
NCBI GI	g1495804
BLAST score	497
E value	4.0e-50
Match length	161
% identity	63
NCBI Description	(X96406) 13-lipoxygenase [Solanum tuberosum]
Seq. No.	29504
Contig ID	193302_1.R1040
5'-most EST	sat701007613.h1
Method	BLASTX
NCBI GI	g3170230
BLAST score	185
E value	7.0e-14
Match length	78
% identity	55
NCBI Description	(AF041848) fructose-6-phosphate 2-kinase /fructose-2,6-bisphosphatase [Spinacia oleracea]
Seq. No.	29505
Contig ID	193348_1.R1040
5'-most EST	jC-gmst02400014b05d1
Method	BLASTX

5'-most EST zhf700965246.h1

Seq. No. 29545
 Contig ID 193951_1.R1040
 5'-most EST bth700845382.h1
 Method BLASTX
 NCBI GI g3241943
 BLAST score 677
 E value 2.0e-71
 Match length 152
 % identity 80
 NCBI Description (AC004625) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29546
 Contig ID 193969_1.R1040
 5'-most EST g5057839

Seq. No. 29547
 Contig ID 193990_1.R1040
 5'-most EST sat701008819.h1

Seq. No. 29548
 Contig ID 193995_1.R1040
 5'-most EST epx701109276.h1
 Method BLASTX
 NCBI GI g4544451
 BLAST score 163
 E value 2.0e-11
 Match length 72
 % identity 46
 NCBI Description (AC006592) unknown protein [Arabidopsis thaliana]

Seq. No. 29549
 Contig ID 194008_1.R1040
 5'-most EST jC-gmro02910067h09a1
 Method BLASTX
 NCBI GI g2245032
 BLAST score 234
 E value 3.0e-19
 Match length 106
 % identity 51
 NCBI Description (Z97342) gibberellin oxidase homolog [Arabidopsis thaliana]

Seq. No. 29550
 Contig ID 194016_1.R1040
 5'-most EST sat701008859.h1

Seq. No. 29551
 Contig ID 194045_1.R1040
 5'-most EST kl1701209619.h1
 Method BLASTX
 NCBI GI g2827556
 BLAST score 169
 E value 3.0e-15
 Match length 127
 % identity 44
 NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]

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Seq. No.      29574
Contig ID     194385_1.R1040
5'-most EST   sat701009379.h1
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09684016

Seq. No.	29602
Contig ID	194900_1.R1040
5'-most EST	jC-gmst02400029f07d1
Method	BLASTX
NCBI GI	g2623297
BLAST score	192
E value	2.0e-14
Match length	59
% identity	56
NCBI Description	(AC002409) unknown p

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Seq. No.                29603
Contig ID               194900_2.R1040
5'-most EST            jC-gmr002910071b07d1
Method                  BLASTX
NCBI-GI -----g2982466 -----
BLAST score             155
E value                 3.0e-10
Match length            39
% identity              59
NCBI Description        (AL022223) putative

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Seq. No.	29605
Contig ID	194930_1.R1040
5'-most EST	sat701010158.h2

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Seq. No.          29607
Contig ID         194946_1.R1040
5'-most EST      sat701010189.h2
Method            BLASTX
NCBI GI           g3695019
BLAST score       297
E value           3.0e-27
Match length      92
```


5'-most EST	jex700904394.h1
Seq. No.	29616
Contig ID	195290_1.R1040
5'-most EST	sat701010670.h1
Seq. No.	29617
Contig ID	195299_1.R1040
5'-most EST	uC-gmrpic019a01b1
Seq. No.	29618
Contig ID	195313_1.R1040
5'-most EST	asn701137390.h1
Method	BLASTX
NCBI GI	g3249105
BLAST score	396
E value	1.0e-38
Match length	98
% identity	69
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]
Seq. No.	29619
Contig ID	195326_1.R1040
5'-most EST	sat701010719.h1
Seq. No.	29620
Contig ID	195354_1.R1040
5'-most EST	asn701138694.h1
Method	BLASTX
NCBI GI	g2342423
BLAST score	274
E value	2.0e-24
Match length	101
% identity	62
NCBI Description	(AB000797) NPK1-related protein kinase 1S [Arabidopsis thaliana]
Seq. No.	29621
Contig ID	195465_1.R1040
5'-most EST	sat701010931.h1
Seq. No.	29622
Contig ID	195499_1.R1040
5'-most EST	sat701010979.h1
Seq. No.	29623
Contig ID	195533_1.R1040
5'-most EST	sat701011065.h1
Method	BLASTX
NCBI GI	g4539314
BLAST score	161
E value	1.0e-11
Match length	54
% identity	57
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

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NCBI GI g4432855
 BLAST score 392
 E value 5.0e-38
 Match length 140
 % identity 68
 NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]

Seq. No. 29631
 Contig ID 195670_1.R1040
 5'-most EST sat701011220.h1

Seq. No. 29632
 Contig ID 195692_1.R1040
 5'-most EST zsg701127909.h1

Seq. No. 29633
 Contig ID 195710_1.R1040
 5'-most EST sat701011269.h1

Seq. No. 29634
 Contig ID 195715_1.R1040
 5'-most EST sat701011275.h1

Seq. No. 29635
 Contig ID 195739_1.R1040
 5'-most EST sat701011311.h1

Seq. No. 29636
 Contig ID 195761_1.R1040
 5'-most EST fua701036962.h1
 Method BLASTX
 NCBI GI g3269296
 BLAST score 145
 E value 5.0e-09
 Match length 76
 % identity 41
 NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 29637
 Contig ID 195771_1.R1040
 5'-most EST jC-gmle01810093d04d1

Seq. No. 29638
 Contig ID 195772_1.R1040
 5'-most EST g4292625
 Method BLASTX
 NCBI GI g4512681
 BLAST score 372
 E value 1.0e-35
 Match length 160
 % identity 52
 NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana]

Seq. No. 29639
 Contig ID 195775_1.R1040
 5'-most EST gsv701050635.h1

Seq. No.	29699
Contig ID	197236_1.R1040
5'-most EST	bth700849379.h1
Method	BLASTX
NCBI GI	g3128176
BLAST score	373
E value	1.0e-35
Match length	118
% identity	55
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.	29700
Contig ID	197237_1.R1040
5'-most EST	gsv701046729.h1
Seq. No.	29701
Contig ID	197355_1.R1040
5'-most EST	sat701013738.h1
Seq. No.	29702
Contig ID	197357_1.R1040
5'-most EST	jC-gmro02910071e07d1
Method	BLASTX
NCBI GI	g2344894
BLAST score	152
E value	7.0e-10
Match length	60
% identity	52
NCBI Description	(AC002388) hypothetical protein [Arabidopsis thaliana]
Seq. No.	29703
Contig ID	197382_1.R1040
5'-most EST	g5606452
Method	BLASTX
NCBI GI	g2275213
BLAST score	473
E value	3.0e-47
Match length	182
% identity	56
NCBI Description	(AC002337) hypothetical protein [Arabidopsis thaliana]
Seq. No.	29704
Contig ID	197403_1.R1040
5'-most EST	uC-gmropic041h04b1
Seq. No.	29705
Contig ID	197406_1.R1040
5'-most EST	jC-gmfl02220053f04a1
Seq. No.	29706
Contig ID	197406_2.R1040
5'-most EST	pxt700944637.h1
Seq. No.	29707
Contig ID	197411_1.R1040
5'-most EST	g5509811
Method	BLASTX

Seq. No.	29771
Contig ID	199039_1.R1040
5'-most EST	awf700842414.h1

Seq. No.	29772
Contig ID	199056_1.R1040
5'-most EST	awf700836959.h1

Seq. No.	29773
Contig ID	199075_1.R1040
5'-most EST	jC-qmst02400026d02a1

Seq. No.	29774
Contig ID	199081_1.R1040
5'-most EST	zhf700953761.h1

Seq. No.	29775
Contig ID	199151_1.R1040
5'-most EST	uC-qmröpic113a07b1

Seq. No.	29776
Contig ID	199167_1.R1040
5'-most EST	awf700837156.h1

Seq. No.	29777
Contig ID	199186_1.R1040
5'-most EST	awf700837147.h1

Seq. No.	29778
Contig ID	199260_1.R1040
5'-most EST	awf700837255.h1

Seq. No.	29779
Contig ID	199274_1.R1040
5'-most EST	awf700837280.h1

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Seq. No.          29780
Contig ID         199297_1.R1040
5'-most EST      jC-gmst02400016e07a1
Method            BLASTX
NCBI GI           g4490708
BLAST score       214
E value           2.0e-17
Match length      51
% identity        80
NCBI Description  (AL035680) putative protein [Arabidopsis thaliana]
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Seq. No.      29781
Contig ID     199312_1.R1040
5'-most EST   jC-gmfl02220104h04d1
Method        BLASTN
NCBI GI       g18731
BLAST score    194
E value        1.0e-105
Match length   218
% identity     97
NCBI Description Soybean RPB1-B1 gene for the largest subunit of RNA
```


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Seq. No.	29783
Contig ID	199315_1.R1040
5'-most EST	crh700852559.h1
Method	BLASTX
NCBI GI	g1363749
BLAST score	152
E value	5.0e-10
Match length	93
% identity	35
NCBI Description	probable membran

Seq. No.	29784
Contig ID	199383_1.R1040
5'-most EST	awf700837445.h1

Seq. No.	29786
Contig ID	199451_1.R1040
5'-most EST	dpv701098501.h1

Seq. No.	29788
Contig ID	199482.1.R1040
5'-most EST	hrw701059258.h1

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Seq. No.      29790
Contig ID     199498_1.R1040
5'-most EST  k11701213363.h1
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Seq. No.          29792
Contig ID         199531_1.R1040
5'-most EST      uC-gmfIminsoyl18d07b1
Method            BLASTX
NCBI GI           g2459421
BLAST score       248
```


BLAST score 145
 E value 3.0e-09
 Match length 118
 % identity 31
 NCBI Description (D90909) extragenic suppressor [Synechocystis sp.]

Seq. No. 29802
 Contig ID 200013_1.R1040
 5'-most EST awf700838363.h1
 Method BLASTN
 NCBI GI g3413510
 BLAST score 77
 E value 2.0e-35
 Match length 197
 % identity 85
 NCBI Description Spinacia oleracea mRNA (nuclear-encoded) for chloroplast glucose-6-phosphate isomerase

Seq. No. 29803
 Contig ID 200043_1.R1040
 5'-most EST awf700838485.h1
 Method BLASTX
 NCBI GI g3063693
 BLAST score 301
 E value 8.0e-28
 Match length 78
 % identity 64
 NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 29804
 Contig ID 200080_1.R1040
 5'-most EST crh700852040.h1
 Method BLASTX
 NCBI GI g135406
 BLAST score 390
 E value 4.0e-38
 Match length 91
 % identity 85
 NCBI Description TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir_A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No. 29805
 Contig ID 200088_1.R1040
 5'-most EST awf700838455.h1

Seq. No. 29806
 Contig ID 200103_1.R1040
 5'-most EST jC-gmle01810008d10a1

Seq. No. 29807
 Contig ID 200188_1.R1040
 5'-most EST awf700839224.h1

Seq. No. 29808
 Contig ID 200237_1.R1040

00000000000000000000000000000000

Seq. No.	29841
Contig ID	201155_1.R1040
5'-most EST	k11701213171.h1
Method	BLASTX
NCBI GI	q4539005

Contig ID 201494_1.R1040
5'-most EST awf700840829.h1

Seq. No. 29850
Contig ID 201523_1.R1040
5'-most EST fC-gmse700840889f1
Method BLASTX
NCBI GI g2708745
BLAST score 694
E value 2.0e-73
Match length 148
% identity 90
NCBI Description (AC003952) putative calcium-dependent ser/thr protein kinase [Arabidopsis thaliana]

Seq. No. 29851
Contig ID 201596_1.R1040
5'-most EST awf700841048.h1

Seq. No. 29852
Contig ID 201650_1.R1040
5'-most EST g5607054
Method BLASTX
NCBI GI g4455358
BLAST score 198
E value 6.0e-15
Match length 75
% identity 52
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 29853
Contig ID 201728_1.R1040
5'-most EST awf700842888.h1

Seq. No. 29854
Contig ID 201752_1.R1040
5'-most EST all700863237.h1
Method BLASTX
NCBI GI g2853087
BLAST score 171
E value 3.0e-12
Match length 105
% identity 41
NCBI Description (AL021768) putative protein [Arabidopsis thaliana]

Seq. No. 29855
Contig ID 201813_1.R1040
5'-most EST kl1701214532.h1
Method BLASTX
NCBI GI g4544422
BLAST score 655
E value 7.0e-69
Match length 144
% identity 44
NCBI Description (AC006955) putative fimbrin [Arabidopsis thaliana]

Seq. No. 29856

Contig ID 201845_1.R1040
 5'-most EST bth700848401.h1
 Method BLASTX
 NCBI GI g4512685
 BLAST score 301
 E value 2.0e-27
 Match length 117
 % identity 49
 NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana]
 >gi_4559325_gb_AAD22987.1 AC007087_6 (AC007087)
 hypothetical protein [Arabidopsis thaliana]

Seq. No. 29857
 Contig ID 201887_1.R1040
 5'-most EST awf700842954.h1

Seq. No. 29858
 Contig ID 201896_1.R1040
 5'-most EST awf700841536.h1

Seq. No. 29859
 Contig ID 201899_1.R1040
 5'-most EST zsg701119244.h1
 Method BLASTX
 NCBI GI g1778376
 BLAST score 373
 E value 5.0e-36
 Match length 104
 % identity 71
 NCBI Description (U81288) PsRT17-1 [Pisum sativum]

Seq. No. 29860
 Contig ID 202021_1.R1040
 5'-most EST pmv700890618.h1

Seq. No. 29861
 Contig ID 202037_1.R1040
 5'-most EST awf700841816.h1

Seq. No. 29862
 Contig ID 202045_1.R1040
 5'-most EST all700863107.h1
 Method BLASTX
 NCBI GI g2462750
 BLAST score 316
 E value 3.0e-29
 Match length 80
 % identity 72
 NCBI Description (AC002292) Highly similar to auxin-induced protein
 (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 29863
 Contig ID 202071_1.R1040
 5'-most EST jC-gmst02400073g02a1

Seq. No. 29864
 Contig ID 202174_1.R1040

0000016390

BLAST score 669
 E value 2.0e-70
 Match length 165
 % identity 75
 NCBI Description (AF004215) ethylene-insensitive3-like3 [Arabidopsis thaliana]

Seq. No. 29894
 Contig ID 203019_1.R1040
 5'-most EST awf700843274.h1

Seq. No. 29895
 Contig ID 203056_1.R1040
 5'-most EST fC-gmse700843342f1
 Method BLASTX
 NCBI GI g3024425
 BLAST score 417
 E value 3.0e-41
 Match length 101
 % identity 80
 NCBI Description PYRUVATE, PHOSPHATE DIKINASE PRECURSOR
 (PYRUVATE, ORTHOPHOSPHATE DIKINASE) >gi_1076700_pir_S53297
 pyruvate, orthophosphate dikinase (EC 2.7.9.1) - Flaveria
 pringlei >gi_577776_emb_CAA53223_(X75516) -
 pyruvate, orthophosphate dikinase [Flaveria pringlei]

Seq. No. 29896
 Contig ID 203103_1.R1040
 5'-most EST awf700843412.h1

Seq. No. 29897
 Contig ID 203167_1.R1040
 5'-most EST yuv700862711.h1

Seq. No. 29898
 Contig ID 203172_1.R1040
 5'-most EST uC-gmröpic071e12b1
 Method BLASTX
 NCBI GI g2781351
 BLAST score 376
 E value 4.0e-36
 Match length 99
 % identity 82
 NCBI Description (AC003113) F2401.7 [Arabidopsis thaliana]

Seq. No. 29899
 Contig ID 203172_2.R1040
 5'-most EST yuv700862718.h1
 Method BLASTX
 NCBI GI g2781351
 BLAST score 193
 E value 7.0e-15
 Match length 52
 % identity 79
 NCBI Description (AC003113) F2401.7 [Arabidopsis thaliana]

Seq. No. 29900

Contig ID 203969_1.R1040
5'-most EST uC-gmrominsoy053g11b1

Seq. No. 29936
Contig ID 203979_1.R1040
5'-most EST pmv700893093.h1
Method BLASTX
NCBI GI g3287695
BLAST score 459
E value 1.0e-45
Match length 142
% identity 56
NCBI Description (AC003979) Similar to hypothetical protein C34B7.2
gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis
thaliana]

Seq. No. 29937
Contig ID 203981_1.R1040
5'-most EST bth700843977.h1
Method BLASTX
NCBI GI g3540207
BLAST score 133
E value 9.0e-16
Match length 70
% identity 59
NCBI Description (AC004260) Putative protein kinase [Arabidopsis thaliana]

Seq. No. 29938
Contig ID 204023_1.R1040
5'-most EST fC-gmro700844046f1
Method BLASTX
NCBI GI g4371296
BLAST score 269
E value 2.0e-23
Match length 107
% identity 53
NCBI Description (AC006260) putative receptor protein kinase [Arabidopsis
thaliana]

Seq. No. 29939
Contig ID 204035_1.R1040
5'-most EST hrw701058057.h1
Method BLASTX
NCBI GI g4454468
BLAST score 716
E value 7.0e-76
Match length 182
% identity 74
NCBI Description (AC006234) putative NADH dehydrogenase [Arabidopsis
thaliana]

Seq. No. 29940
Contig ID 204104_1.R1040
5'-most EST dpv701102894.h1

Seq. No. 29941
Contig ID 204152_1.R1040

Seq. No. 29948
 Contig ID 204399_1.R1040
 5'-most EST jC-gmro02910040h01a1

Seq. No. 29949
 Contig ID 204409_1.R1040
 5'-most EST jC-gmle01810073e01a1
 Method BLASTX
 NCBI GI g3549679
 BLAST score 535
 E value 2.0e-54
 Match length 214
 % identity 55
 NCBI Description (AL031394) putative protein [Arabidopsis thaliana]

Seq. No. 29950
 Contig ID 204433_1.R1040
 5'-most EST jC-gmro02910066d05a1
 Method BLASTX
 NCBI GI g3786008
 BLAST score 173
 E value 4.0e-12
 Match length 186
 % identity 30
 NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 29951
 Contig ID 204467_1.R1040
 5'-most EST bth700845393.h1
 Method BLASTX
 NCBI GI g4105794
 BLAST score 306
 E value 6.0e-28
 Match length 119
 % identity 49
 NCBI Description (AF049928) PGP224 [Petunia x hybrida]

Seq. No. 29952
 Contig ID 204473_1.R1040
 5'-most EST bth700844643.h1

Seq. No. 29953
 Contig ID 204531_1.R1040
 5'-most EST fC-gmro700844719f1
 Method BLASTX
 NCBI GI g1313907
 BLAST score 469
 E value 8.0e-47
 Match length 122
 % identity 72
 NCBI Description (D84507) CDPK-related protein kinase [Zea mays]

Seq. No. 29954
 Contig ID 204563_1.R1040
 5'-most EST jC-gmro02910038d02d1

Seq. No. 29955

5'-most EST	jC-gmle01810012d08a1
Seq. No.	29961
Contig ID	204716_1.R1040
5'-most EST	uC-gmrominsoy176b11b1
Method	BLASTX
NCBI GI	g4415924
BLAST score	403
E value	2.0e-48
Match length	174
% identity	57
NCBI Description	(AC006282) putative glucosyl transferase [Arabidopsis thaliana]
Seq. No.	29962
Contig ID	204718_1.R1040
5'-most EST	leu701155225.h1
Method	BLASTX
NCBI GI	g3367522
BLAST score	284
E value	2.0e-25
Match length	102
% identity	52
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]
Seq. No.	29963
Contig ID	204731_1.R1040
5'-most EST	uC-gmflminsoy016b12b1
Method	BLASTX
NCBI GI	g2191136
BLAST score	289
E value	5.0e-26
Match length	131
% identity	50
NCBI Description	(AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]
Seq. No.	29964
Contig ID	204764_1.R1040
5'-most EST	dpv701101540.h1
Seq. No.	29965
Contig ID	204773_1.R1040
5'-most EST	leu701156438.h1
Seq. No.	29966
Contig ID	204791_1.R1040
5'-most EST	kl1701207611.h1
Method	BLASTX
NCBI GI	g2459441
BLAST score	315
E value	5.0e-30
Match length	108
% identity	64

NCBI Description (AC002332) putative SWI/SNF complex subunit BAF170
[Arabidopsis thaliana]

Seq. No. 29967
Contig ID 204791_2.R1040
5'-most EST fua701037770.h1

Seq. No. 29968
Contig ID 204793_1.R1040
5'-most EST g5126294

Seq. No. 29969
Contig ID 204811_1.R1040
5'-most EST g4286952

Seq. No. 29970
Contig ID 204818_1.R1040
5'-most EST zsg701118888.h1

Seq. No. 29971
Contig ID 204852_1.R1040
5'-most EST bth700846660.h1
Method BLASTX

NCBI GI g4467156

BLAST score 170

E value 2.0e-12

Match length 56

% identity 62

NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 29972
Contig ID 204862_1.R1040
5'-most EST bth700848868.h1

Method BLASTN

NCBI GI g3005575

BLAST score 169

E value 1.0e-89

Match length 397

% identity 86

NCBI Description Glycine max putative high affinity nitrate transporter
(NRT2) mRNA, complete cds

Seq. No. 29973
Contig ID 204866_1.R1040
5'-most EST jC-gmro02910008f11a1

Method BLASTX

NCBI GI g2746086

BLAST score 504

E value 4.0e-51

Match length 159

% identity 65

NCBI Description (AF025292) putative high-affinity potassium transporter
[Hordeum vulgare]

Seq. No. 29974
Contig ID 204870_1.R1040
5'-most EST bth700845152.h1

[illegible][illegible]

TOTAL

[illegible]

TOTAL

[illegible][illegible][illegible]

SECRET

Seq. No. 30019

Seq. No. 30028
 Contig ID 206185_1.R1040
 5'-most EST bth700846826.h1

Seq. No. 30029
 Contig ID 206227_1.R1040
 5'-most EST pmv700890991.h1

Seq. No. 30030
 Contig ID 206230_1.R1040
 5'-most EST jC-gmro02910068h01a1

Seq. No. 30031
 Contig ID 206233_1.R1040
 5'-most EST pxt700942737.h1
 Method BLASTX
 NCBI GI g2947063
 BLAST score 429
 E value 5.0e-42
 Match length 176
 % identity 51
 NCBI Description (AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No. 30032
 Contig ID 206300_1.R1040
 5'-most EST fua701039394.h1
 Method BLASTX
 NCBI GI g4263818
 BLAST score 295
 E value 2.0e-26
 Match length 184
 % identity 38
 NCBI Description (AC006067) unknown protein [Arabidopsis thaliana]

Seq. No. 30033
 Contig ID 206355_1.R1040
 5'-most EST jC-gmro02800030g03a1
 Method BLASTX
 NCBI GI g4063742
 BLAST score 306
 E value 1.0e-27
 Match length 116
 % identity 56
 NCBI Description (AC005851) putative phaseolin G-box binding protein [Arabidopsis thaliana]

Seq. No. 30034
 Contig ID 206370_1.R1040
 5'-most EST jC-gmle01810042c10a1

Seq. No. 30035
 Contig ID 206426_1.R1040
 5'-most EST bth700847167.h1
 Method BLASTX
 NCBI GI g3341694

% identity 88
 NCBI Description (AF128392) No definition line found [Arabidopsis thaliana]

Seq. No. 30046
 Contig ID 206591_1.R1040
 5'-most EST bth700847364.h1
 Method BLASTX
 NCBI GI g4335745
 BLAST score 223
 E value 4.0e-18
 Match length 98
 % identity 43
 NCBI Description (AC006284) putative hydrolase (contains an
 esterase/lipase/thioesterase active site serine domain
 (prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 30047
 Contig ID 206653_1.R1040
 5'-most EST jex700907913.h1

Seq. No. 30048
 Contig ID 206675_1.R1040
 5'-most EST jC-gmle01810077e06d1

Seq. No. 30049
 Contig ID 206691_1.R1040
 5'-most EST pmv700893634.h1
 Method BLASTX
 NCBI GI g2827630
 BLAST score 295
 E value 7.0e-39
 Match length 109
 % identity 72
 NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 30050
 Contig ID 206700_1.R1040
 5'-most EST fua701040870.h1
 Method BLASTX
 NCBI GI g2829887
 BLAST score 282
 E value 2.0e-25
 Match length 87
 % identity 61
 NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 30051
 Contig ID 206726_1.R1040
 5'-most EST uC-gmrominsoy193g08b1
 Method BLASTX
 NCBI GI g3335060
 BLAST score 293
 E value 2.0e-28
 Match length 97
 % identity 74
 NCBI Description (AF025842) plasma membrane-type calcium ATPase [Arabidopsis
 thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma

0000010986

NCBI Description (AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	30114
Contig ID	207903_1.R1040
5'-most EST	jC-qmst02400001f09a1

NCBI Description CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE)
(O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
>gi_1071911_pir_S46438 cysteine synthase (EC 4.2.99.8) -
watermelon >gi_540497_dbj_BAA05965_ (D28777) cysteine
synthase [Citrus limon]

NCBI Description (AJ006024) cysteine synthase, O-acetyl-L-serine (thiol)-lyase [Cicer arietinum]

Seq. No.	30118
Contig ID	207907 1.R1040

00000000000000000000000000000000

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Seq. No.          30120
Contig ID         207919_1.R1040
5'-most EST      uC-gmf1minsoy017e02b1
Method            BLASTX
NCBI GI           g4191786
BLAST score       592
E value           2.0e-61
Match length      163
% identity        71
NCBI Description  (AC005917) unknown protein [Arabidopsis thaliana]
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Seq. No.          30121
Contig ID         207968_1.R1040
5'-most EST      fua701040728.h1
Method            BLASTX
NCBI GI           g2829864
BLAST score       154
E value           2.0e-10
Match length      45
% identity        60
NCBI Description  (AC002396) similar to zinc metalloproteinases [Arabidopsis
                  thaliana]
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Seq. No.          30122
Contig ID         207983_1.R1040
5'-most EST      uC-gmröpic043g07b1
Method            BLASTX
NCBI GI           g3668087
BLAST score       518
E value           1.0e-52
Match length      161
% identity        38
NCBI Description  (AC004667) hypothetical protein [Arabidopsis thaliana]
```

Seq. No.	30123
Contig ID	208017_1.R1040
5'-most EST	bth700849224.h1

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Seq. No.          30124
Contig ID         208024_1.R1040
5'-most EST      bth700849231.h1
Method            BLASTX
NCBI GI           g2252847
BLAST score       173
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Seq. No. 30165
 Contig ID 208930_1.R1040
 5'-most EST jex700903610.h1

Seq. No. 30166
 Contig ID 208955_1.R1040
 5'-most EST jex700903642.h1
 Method BLASTX
 NCBI GI g4455246
 BLAST score 188
 E value 5.0e-14
 Match length 94
 % identity 50
 NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 30167
 Contig ID 208969_1.R1040
 5'-most EST jex700903674.h1

Seq. No. 30168
 Contig ID 208971_1.R1040
 5'-most EST zsg701123853.h1
 Method BLASTX
 NCBI GI g1711618
 BLAST score 444
 E value 4.0e-44
 Match length 126
 % identity 69
 NCBI Description LOW AFFINITY SULPHATE TRANSPORTER 3 >gi_1085993_pir_S51765
 low affinity sulphate transporter - Stylosanthes hamata
 >gi_607188_emb_CAA57831_(X82454) low affinity sulphate
 transporter [Stylosanthes hamata]

Seq. No. 30169
 Contig ID 208991_1.R1040
 5'-most EST fC-gmf1700904235a1
 Method BLASTX
 NCBI GI g3047095
 BLAST score 272
 E value 7.0e-24
 Match length 109
 % identity 30
 NCBI Description (AF058826) similar to eukaryotic protein kinase domains
 (Pfam: pkinase.hmm, score: 72.39) [Arabidopsis thaliana]

Seq. No. 30170
 Contig ID 209019_1.R1040
 5'-most EST fC-gmf1700903761f4
 Method BLASTX
 NCBI GI g1150406
 BLAST score 293
 E value 3.0e-26
 Match length 142
 % identity 43
 NCBI Description (Z46868) exo-1,3-beta-glucanase/1,3-beta-D-glucan
 glucanohydrolase [Pichia angusta]

Seq. No. 30171
Contig ID 209026_1.R1040
5'-most EST leu701149594.h1

Seq. No. 30172
Contig ID 209044_1.R1040
5'-most EST jex700906355.h1

Seq. No. 30173
Contig ID 209057_1.R1040
5'-most EST jex700903826.h1

Seq. No. 30174
Contig ID 209062_1.R1040
5'-most EST jC-gmro02910004g06a1

Seq. No. 30175
Contig ID 209078_1.R1040
5'-most EST jex700903873.h1

Seq. No. 30176
Contig ID 209094_1.R1040
5'-most EST jex700903894.h1

Seq. No. 30177
Contig ID 209127_1.R1040
5'-most EST uC-gmropic010c06b1
Method BLASTX
NCBI GI g1297187
BLAST score 654
E value 2.0e-68
Match length 212
% identity 60
NCBI Description (U53501) similar to protein encoded by GenBank Accession Number U41815, nucleoporin 98 [Arabidopsis thaliana]

Seq. No. 30178
Contig ID 209142_1.R1040
5'-most EST jex700904010.h1

Seq. No. 30179
Contig ID 209146_1.R1040
5'-most EST jex700904018.h1

Seq. No. 30180
Contig ID 209173_1.R1040
5'-most EST uC-gmflminsoy012g11b1
Method BLASTX
NCBI GI g2576361
BLAST score 568
E value 1.0e-58
Match length 138
% identity 74
NCBI Description (U39782) lysine and histidine specific transporter [Arabidopsis thaliana]

Contig ID	209566_1.R1040
5'-most EST	uC-gmropic022a02b1
Seq. No.	30197
Contig ID	209574_1.R1040
5'-most EST	zhf700958011.h1
Method	BLASTX
NCBI GI	g99808
BLAST score	570
E value	9.0e-59
Match length	171
% identity	63
NCBI Description	gene Bp10.protein - rape >gi_17797_emb_CAA47178_ (X66609) Bplo [Brassica napus]
Seq. No.	30198
Contig ID	209577_1.R1040
5'-most EST	jC-gmfl02220142h02a1
Seq. No.	30199
Contig ID	209616_1.R1040
5'-most EST	jC-gmfl02220100e08a1
Method	BLASTX
NCBI GI	g1708972
BLAST score	217
E value	3.0e-17
Match length	101
% identity	50
NCBI Description	(R)-MANDELONITRILE LYASE ISOFORM 3 PRECURSOR (HYDROXYNITRILE LYASE 3) ((R)-OXYNITRILASE 3) >gi_1262279 (U51562) (R)-(+)-mandelonitrile lyase isoform MDL3 precursor [Prunus serotina] >gi_2343181 (AF013161) (R)-(+)-mandelonitrile lyase isoform MDL3 precursor [Prunus serotina]
Seq. No.	30200
Contig ID	209640_1.R1040
5'-most EST	k11701205153.h1
Seq. No.	30201
Contig ID	209667_1.R1040
5'-most EST	jex700904771.h1
Method	BLASTX
NCBI GI	g4455171
BLAST score	751
E value	6.0e-80
Match length	196
% identity	66
NCBI Description	(AL035521) hypothetical protein [Arabidopsis thaliana]
Seq. No.	30202
Contig ID	209683_1.R1040
5'-most EST	leu701149039.h1
Seq. No.	30203
Contig ID	209717_1.R1040
5'-most EST	leu701153716.h1

Method BLASTX
 NCBI GI g2842496
 BLAST score 448
 E value 2.0e-44
 Match length 121
 % identity 73
 NCBI Description (AL021749) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No. 30204
 Contig ID 209723_1.R1040
 5'-most EST jex700904868.h1
 Method BLASTX
 NCBI GI g4415912
 BLAST score 148
 E value 8.0e-10
 Match length 85
 % identity 35
 NCBI Description (AC006282) putative protease [Arabidopsis thaliana]

Seq. No. 30205
 Contig ID 209745_1.R1040
 5'-most EST gsv701051266.h1
 Method BLASTX
 NCBI GI g4559320
 BLAST score 278
 E value 8.0e-25
 Match length 100
 % identity 52
 NCBI Description (AC007087) putative 50S ribosomal protein L1 [Arabidopsis thaliana]

Seq. No. 30206
 Contig ID 209767_1.R1040
 5'-most EST jex700904935.h1
 Method BLASTX
 NCBI GI g2114104
 BLAST score 341
 E value 1.0e-64
 Match length 178
 % identity 71
 NCBI Description (AB003590) sulfate transporter [Arabidopsis thaliana]
 >gi_2114106_dbj_BAA20085_ (AB003591) sulfate transporter
 [Arabidopsis thaliana]

Seq. No. 30207
 Contig ID 209780_1.R1040
 5'-most EST jex700905528.h1

Seq. No. 30208
 Contig ID 209808_1.R1040
 5'-most EST jex700904983.h1
 Method BLASTX
 NCBI GI g4008008
 BLAST score 251
 E value 2.0e-21
 Match length 93
 % identity 56

NCBI Description (AF084035) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 30209
 Contig ID 209826_1.R1040
 5'-most EST jC-gmro02910010e04a1

Seq. No. 30210
 Contig ID 209832_1.R1040
 5'-most EST jC-gmst02400044b04a1
 Method BLASTX
 NCBI GI g3885344
 BLAST score 172
 E value 4.0e-12
 Match length 126
 % identity 34
 NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]
 >gi_4557057_gb_AAD22497.1_AC007154_1 (AC007154) unknown protein [Arabidopsis thaliana]

Seq. No. 30211
 Contig ID 209864_1.R1040
 5'-most EST jex700905078.h1

Seq. No. 30212
 Contig ID 209902_1.R1040
 5'-most EST jC-gmfl02220099h10d1

Seq. No. 30213
 Contig ID 209926_1.R1040
 5'-most EST fC-gmfl700906103a1

Seq. No. 30214
 Contig ID 209939_1.R1040
 5'-most EST jC-gmro02910047b05a1
 Method BLASTX
 NCBI GI g4539335
 BLAST score 375
 E value 1.0e-35
 Match length 249
 % identity 35
 NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 30215
 Contig ID 209939_2.R1040
 5'-most EST uC-gmrominsoy302e03b1
 Method BLASTX
 NCBI GI g4539335
 BLAST score 243
 E value 1.0e-20
 Match length 137
 % identity 39
 NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 30216
 Contig ID 209949_1.R1040
 5'-most EST zhf700955913.h1

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Method BLASTX
 NCBI GI g2126113
 BLAST score 169
 E value 1.0e-11
 Match length 116
 % identity 36
 NCBI Description prolyl aminopeptidase (EC 3.4.11.5) - Hafnia alvei
 >gi_1754489_dbj_BAA09605_(D61383) prolyl aminopeptidase
 [Hafnia alvei] >gi_1588323_prf__2208340A Pro aminopeptidase
 [Hafnia alvei]

Seq. No. 30277
 Contig ID 211346_1.R1040
 5'-most EST leu701148125.h1

Seq. No. 30278
 Contig ID 211382_1.R1040
 5'-most EST kl1701209577.h1
 Method BLASTX
 NCBI GI g4006915
 BLAST score 332
 E value 3.0e-31
 Match length 107
 % identity 61
 NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30279
 Contig ID 211394_1.R1040
 5'-most EST jex700907530.h1
 Method BLASTX
 NCBI GI g2781433
 BLAST score 246
 E value 7.0e-21
 Match length 131
 % identity 40
 NCBI Description (AF030052) RSW1-like cellulose synthase catalytic subunit
 [Oryza sativa subsp. japonica]

Seq. No. 30280
 Contig ID 211399_1.R1040
 5'-most EST jC-gmst02400076g02a1
 Method BLASTX
 NCBI GI g4115379
 BLAST score 277
 E value 2.0e-24
 Match length 123
 % identity 54
 NCBI Description (AC005967) putative carbonyl reductase [Arabidopsis
 thaliana]

Seq. No. 30281
 Contig ID 211442_1.R1040
 5'-most EST zsg701118392.h1
 Method BLASTX
 NCBI GI g2911067
 BLAST score 585
 E value 1.0e-60

Match length 137
 % identity 81
 NCBI Description (AL021960) UV-damaged DNA-binding protein- like
 [Arabidopsis thaliana]

Seq. No. 30282
 Contig ID 211471_1.R1040
 5'-most EST leu701152212.h1
 Method BLASTX
 NCBI GI g1931652
 BLAST score 221
 E value 9.0e-18
 Match length 188
 % identity 18
 NCBI Description (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog
 [Arabidopsis thaliana]

Seq. No. 30283
 Contig ID 211583_1.R1040
 5'-most EST epx701106685.h1

Seq. No. 30284
 Contig ID 211591_1.R1040
 5'-most EST leu701145967.h1
 Method BLASTX
 NCBI GI g2642157
 BLAST score 201
 E value 3.0e-19
 Match length 69
 % identity 70
 NCBI Description (AC003000) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 30285
 Contig ID 211626_1.R1040
 5'-most EST fC-gmro700876145d1
 Method BLASTN
 NCBI GI g1089903
 BLAST score 56
 E value 1.0e-22
 Match length 128
 % identity 86
 NCBI Description P.sativum mRNA for carboxypeptidase

Seq. No. 30286
 Contig ID 211644_1.R1040
 5'-most EST zhf700963153.h1
 Method BLASTX
 NCBI GI g2655008
 BLAST score 600
 E value 3.0e-62
 Match length 186
 % identity 55
 NCBI Description (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon
 esculentum]

Seq. No. 30287
 Contig ID 211656_1.R1040

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Seq. No.          30289
Contig ID         211732_1.R1040
5'-most EST      leu701149360.h1
Method            BLASTX
NCBI GI           g4559368
BLAST score       213
E value           2.0e-17
Match length      58
% identity        72
NCBI Description  (AC006585) hypothetical protein [Arabidopsis thaliana]
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Seq. No.          30291
Contig ID         211924_1.R1040
5'-most EST      leu701150702.h1
Method            BLASTX
NCBI GI           g4218120
BLAST score       167
E value           6.0e-12
Match length      43
% identity        77
NCBI Description  (AL035353) Proline-rich APG-like protein [Arabidopsis
                  thaliana]
```

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NCBI GI g1345643
 BLAST score 419
 E value 5.0e-49
 Match length 138
 % identity 74
 NCBI Description FLAVONOID 3',5'-HYDROXYLASE 2 (F3'5'H) (CYTOCHROME P450 75A3) (CYPLXXVA3) >gi_629709_pir_S38984 flavonoid 3',5'-hydroxylase Hf2 - garden petunia >gi_311654_emb_CAA80265_ (Z22544) flavonoid 3',5'-hydroxylase [Petunia x hybrida] >gi_738771_prf_2001426A flavonoid 3',5'-hydroxylase [Petunia x hybrida]

Seq. No. 30307
 Contig ID 212108_1.R1040
 5'-most EST pxt700944644.h1
 Method BLASTX
 NCBI GI g1871193
 BLAST score 424
 E value 1.0e-42
 Match length 163
 % identity 52
 NCBI Description (U90439) receptor-like protein kinase isolog [Arabidopsis thaliana] >gi_2335090 (AC002339) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 30308
 Contig ID 212118_1.R1040
 5'-most EST jex700908656.h1

Seq. No. 30309
 Contig ID 212134_1.R1040
 5'-most EST zhf700954902.h1

Seq. No. 30310
 Contig ID 212181_1.R1040
 5'-most EST jex700909274.h1
 Method BLASTX
 NCBI GI g3687230
 BLAST score 637
 E value 1.0e-66
 Match length 163
 % identity 70
 NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30311
 Contig ID 212187_1.R1040
 5'-most EST g5510128
 Method BLASTX
 NCBI GI g4530126
 BLAST score 227
 E value 1.0e-18
 Match length 90
 % identity 51
 NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

NCBI Description (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No. 30321
Contig ID 212315_1.R1040
5'-most EST uC-gmrominsoy220g05b1

Seq. No. 30322
Contig ID 212323_1.R1040
5'-most EST jex700908953.h1
Method BLASTX
NCBI GI g4105698
BLAST score 171
E value 2.0e-12
Match length 66
% identity 52
NCBI Description (AF049870) small hydrophobic protein [Arabidopsis thaliana]

Seq. No. 30323
Contig ID 212331_1.R1040
5'-most EST kl1701214360.h1
Method BLASTX
NCBI GI g4522012
BLAST score 546
E value 8.0e-56
Match length 185
% identity 57
NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30324
Contig ID 212379_1.R1040
5'-most EST uC-gmrominsoy158a10b1

Seq. No. 30325
Contig ID 212408_1.R1040
5'-most EST fC-gmse700755370a2

Seq. No. 30326
Contig ID 212416_1.R1040
5'-most EST jC-gmro02910013e12a1
Method BLASTX
NCBI GI g2252472
BLAST score 813
E value 3.0e-87
Match length 182
% identity 85
NCBI Description (Z97558) argininosuccinate lyase [Arabidopsis thaliana]

Seq. No. 30327
Contig ID 212437_1.R1040
5'-most EST gsv701056350.h1
Method BLASTX
NCBI GI g1076580
BLAST score 223
E value 3.0e-18
Match length 75
% identity 56
NCBI Description alcohol dehydrogenase homolog ADH3b - tomato

5'-most EST zhf700951787.h1
 Method BLASTX
 NCBI GI g2246458
 BLAST score 165
 E value 2.0e-11
 Match length 41
 % identity 76
 NCBI Description (U81313) S-adenosyl-methionine-sterol-C- methyltransferase
 [Ricinus communis]

Seq. No. 30375
 Contig ID 213150_2.R1040
 5'-most EST jC-gmle01810004e10a1
 Method BLASTN
 NCBI GI g1399379
 BLAST score 108
 E value 1.0e-53
 Match length 268
 % identity 85
 NCBI Description Glycine max S-adenosyl-L-methionine:delta24-sterol-C-
 methyltransferase mRNA, complete cds

Seq. No. 30376
 Contig ID 213155_1.R1040
 5'-most EST zhf700951794.h1

Seq. No. 30377
 Contig ID 213203_1.R1040
 5'-most EST zhf700962818.h1

Seq. No. 30378
 Contig ID 213233_1.R1040
 5'-most EST zhf700951901.h1
 Method BLASTX
 NCBI GI g3335350
 BLAST score 122
 E value 3.0e-14
 Match length 84
 % identity 51
 NCBI Description (AC004512) Similar to gb_Z84386 anthranilate
 N-hydroxycinnamoyl/benzoyltransferase from Dianthus
 caryophyllus. [Arabidopsis thaliana]

Seq. No. 30379
 Contig ID 213290_1.R1040
 5'-most EST leu701154862.h1

Seq. No. 30380
 Contig ID 213302_1.R1040
 5'-most EST jC-gmr002910016b06a1

Seq. No. 30381
 Contig ID 213338_1.R1040
 5'-most EST zhf700952049.h1

Seq. No. 30382
 Contig ID 213339_1.R1040

Contig ID 213519_1.R1040
 5'-most EST zhf700952272.h1
 Method BLASTX
 NCBI GI g2623248
 BLAST score 264
 E value 3.0e-25
 Match length 93
 % identity 68
 NCBI Description (AF030882) SU1 isoamylase [Zea mays]

Seq. No. 30391
 Contig ID 213533_1.R1040
 5'-most EST uC-gmflminsoy058f04b1

Seq. No. 30392
 Contig ID 213537_1.R1040
 5'-most EST zhf700952301.h1
 Method BLASTX
 NCBI GI g1351945
 BLAST score 177
 E value 3.0e-22
 Match length 107
 % identity 59
 NCBI Description FLORAL HOMEOTIC PROTEIN APETALA2 >gi_533709 (U12546)
 APETALA2 protein [Arabidopsis thaliana]
 >gi_2464888_emb_CAB16765_ (Z99707) APETALA2 protein
 [Arabidopsis thaliana]

Seq. No. 30393
 Contig ID 213598_1.R1040
 5'-most EST zhf700952364.h1
 Method BLASTN
 NCBI GI g2330650
 BLAST score 49
 E value 2.0e-18
 Match length 205
 % identity 90
 NCBI Description Pisum sativum mRNA for topoisomerase II

Seq. No. 30394
 Contig ID 213627_1.R1040
 5'-most EST zhf700952402.h1

Seq. No. 30395
 Contig ID 213640_1.R1040
 5'-most EST g4313837
 Method BLASTX
 NCBI GI g3738297
 BLAST score 487
 E value 2.0e-49
 Match length 111
 % identity 31
 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 30396
 Contig ID 213655_1.R1040
 5'-most EST fua701037671.h1

BLAST score	211
E value	1.0e-22
Match length	140
% identity	43
NCBI Description	(AC005770) unknown protein, 5' partial [Arabidopsis thaliana]
Seq. No.	30416
Contig ID	214017_1.R1040
5'-most EST	zhf700963236.h1
Seq. No.	30417
Contig ID	214022_1.R1040
5'-most EST	gsv701055630.h1
Seq. No.	30418
Contig ID	214035_1.R1040
5'-most EST	uC-gmflminsoy017f01b1
Seq. No.	30419
Contig ID	214057_1.R1040
5'-most EST	zhf700953006.h1
Method	BLASTX
NCBI GI	g2245070
BLAST score	150
E value	2.0e-09
Match length	167
% identity	28
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]
Seq. No.	30420
Contig ID	214099_1.R1040
5'-most EST	zhf700953069.h1
Method	BLASTX
NCBI GI	g3075382
BLAST score	320
E value	6.0e-30
Match length	82
% identity	77
NCBI Description	(AC002505) putative peroxisome assembly protein PER8 [Arabidopsis thaliana] >gi_3075384 (AC004484) putative peroxisome assembly protein PER8 [Arabidopsis thaliana]
Seq. No.	30421
Contig ID	214157_1.R1040
5'-most EST	uC-gmronoir009a11b1
Seq. No.	30422
Contig ID	214160_1.R1040
5'-most EST	zhf700964709.h1
Method	BLASTX
NCBI GI	g3415115
BLAST score	542
E value	1.0e-55
Match length	131
% identity	39
NCBI Description	(AF081202) villin 2 [Arabidopsis thaliana]

Seq. No. 30423
 Contig ID 214172_1.R1040
 5'-most EST uC-gmronoir071g02b1
 Method BLASTX
 NCBI GI g2911058
 BLAST score 317
 E value 8.0e-29
 Match length 145
 % identity 42
 NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 30424
 Contig ID 214210_1.R1040
 5'-most EST epX701103943.h1
 Method BLASTX
 NCBI GI g3980401
 BLAST score 189
 E value 1.0e-20
 Match length 78
 % identity 55
 NCBI Description (AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No. 30425
 Contig ID 214227_1.R1040
 5'-most EST uC-gmropic042a01b1

Seq. No. 30426
 Contig ID 214227_2.R1040
 5'-most EST kl1701206481.h1

Seq. No. 30427
 Contig ID 214229_1.R1040
 5'-most EST zhf700953234.h1

Seq. No. 30428
 Contig ID 214259_1.R1040
 5'-most EST jC-gmst02400076e02a1
 Method BLASTX
 NCBI GI g3201624
 BLAST score 220
 E value 1.0e-17
 Match length 124
 % identity 56
 NCBI Description (AC004669) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30429
 Contig ID 214261_1.R1040
 5'-most EST uC-gmflminsoy020b01b1

Seq. No. 30430
 Contig ID 214263_1.R1040
 5'-most EST zhf700953279.h1

Seq. No. 30431
 Contig ID 214278_1.R1040

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Seq. No.	30449
Contig ID	214526_1.R1040
5'-most EST	jC-qmf102220136h02d1

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Seq. No.          30451
Contig ID         214623.1.R1040
5'-most EST      kl1701210714.h1
Method            BLASTX
NCBI GI           g3953475
BLAST score       275
E value           2.0e-24
Match length      93
% identity        54
NCBI Description  (AC002328) F22O2.20 [Arabidopsis thaliana]
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Seq. No.          30453
Contig ID         214691_1.R1040
5'-most EST      uC-gmrominsoy126e11b1
Method            BLASTN
NCBI GI           g3869069
BLAST score       53
E value           1.0e-20
Match length      230
% identity        83
```

Seq. No.	30454
Contig ID	214720_1.R1040
5'-most EST	jC-qmfl02220143a07a1

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Seq. No.	30479
Contig ID	215276_1.R1040
5'-most EST	leu701145160.h1
Seq. No.	30480
Contig ID	215309_1.R1040
5'-most EST	zhf700954581.h1
Seq. No.	30481
Contig ID	215324_1.R1040
5'-most EST	kl1701213457.h1
Seq. No.	30482
Contig ID	215327_1.R1040
5'-most EST	uC-gmflminsoy044c05b1
Method	BLASTX
NCBI GI	g4204315
BLAST score	234
E value	3.0e-19
Match length	195
% identity	30
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]
Seq. No.	30483
Contig ID	215341_1.R1040
5'-most EST	zsg701117642.h1
Seq. No.	30484
Contig ID	215353_1.R1040
5'-most EST	jC-gmle01810016g02a1
Method	BLASTX
NCBI GI	g1175016
BLAST score	143
E value	1.0e-08
Match length	134
% identity	32
NCBI Description	WHITE PROTEIN HOMOLOG >gi_1160186_emb_CAA62631_ (X91249) white [Homo sapiens]
Seq. No.	30485
Contig ID	215369_1.R1040
5'-most EST	zhf700954654.h1
Seq. No.	30486
Contig ID	215377_1.R1040
5'-most EST	g4313727
Method	BLASTX
NCBI GI	g3258570
BLAST score	172
E value	3.0e-12
Match length	45
% identity	73
NCBI Description	(U89959) Unknown protein [Arabidopsis thaliana]
Seq. No.	30487
Contig ID	215396_1.R1040
5'-most EST	jC-qmst02400029f12a1

Seq. No. 30488
 Contig ID 215433_1.R1040
 5'-most EST zhf700954735.h1
 Method BLASTX
 NCBI GI g4263722
 BLAST score 289
 E value 1.0e-43
 Match length 101
 % identity 88
 NCBI Description (AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No. 30489
 Contig ID 215441_1.R1040
 5'-most EST k11701212167.h1
 Method BLASTX
 NCBI GI g2507229
 BLAST score 329
 E value 1.0e-30
 Match length 93
 % identity 69
 NCBI Description 40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE)
 (ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED
 PROTEIN) (ESTROGEN RECEPTOR BINDING CYCLOPHILIN)
 >gi_423247_pir_A46579 estrogen receptor-binding
 cyclophilin - bovine >gi_393300_dbj_BAA03159_ (D14074)
 cyclophilin [Bos taurus]

Seq. No. 30490
 Contig ID 215446_1.R1040
 5'-most EST fC-gmle7000743383r1

Seq. No. 30491
 Contig ID 215485_1.R1040
 5'-most EST zhf700954794.h1

Seq. No. 30492
 Contig ID 215492_1.R1040
 5'-most EST jC-gmfl02220097f08a1
 Method BLASTX
 NCBI GI g3982577
 BLAST score 295
 E value 4.0e-32
 Match length 102
 % identity 67
 NCBI Description (AF023141) histidinol dehydrogenase [Thlaspi goesingense]

Seq. No. 30493
 Contig ID 215497_1.R1040
 5'-most EST uC-gmropic112d12b1
 Method BLASTX
 NCBI GI g4508076
 BLAST score 190
 E value 2.0e-14
 Match length 96
 % identity 38
 NCBI Description (AC005882) 55659 [Arabidopsis thaliana]

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NCBI Description (AC006592) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30512
 Contig ID 215997_1.R1040
 5'-most EST leu701145993.h1
 Method BLASTX
 NCBI GI g2342685
 BLAST score 336
 E value 2.0e-31
 Match length 126
 % identity 52
 NCBI Description (AC000106) Contains similarity to Rhodococcus amidase (gb_D16207). ESTs gb_T20504, gb_H36650, gb_N97423, gb_H36595 come from this gene. [Arabidopsis thaliana]

Seq. No. 30513
 Contig ID 215997_2.R1040
 5'-most EST jC-gmfl02220061a09a1
 Method BLASTX
 NCBI GI g2342685
 BLAST score 231
 E value 4.0e-19
 Match length 147
 % identity 37
 NCBI Description (AC000106) Contains similarity to Rhodococcus amidase (gb_D16207). ESTs gb_T20504, gb_H36650, gb_N97423, gb_H36595 come from this gene. [Arabidopsis thaliana]

Seq. No. 30514
 Contig ID 216033_1.R1040
 5'-most EST jC-gmro02910072e02a1
 Method BLASTX
 NCBI GI g3776559
 BLAST score 671
 E value 1.0e-70
 Match length 151
 % identity 81
 NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]

Seq. No. 30515
 Contig ID 216037_1.R1040
 5'-most EST zhf700955536.h1

Seq. No. 30516
 Contig ID 216060_1.R1040
 5'-most EST uC-gmflminsoy017a05b1

Seq. No. 30517
 Contig ID 216101_1.R1040
 5'-most EST uC-gmropic065c05b1

Seq. No. 30518
 Contig ID 216111_1.R1040
 5'-most EST zhf700955632.h1

Method	BLASTX
NCBI GI	g3135254
BLAST score	704
E value	3.0e-74
Match length	278
% identity	50
NCBI Description	(AC003058) hypothetical protein [Arabidopsis thaliana]
Seq. No.	30519
Contig ID	216112_1.R1040
5'-most EST	pxt700944059.h1
Method	BLASTX
NCBI GI	g2760839
BLAST score	417
E value	1.0e-40
Match length	175
% identity	47
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]
Seq. No.	30520
Contig ID	216131_1.R1040
5'-most EST	uC-gmrominsoyl112e02b1
Method	BLASTX
NCBI GI	g2252843
BLAST score	482
E value	1.0e-48
Match length	147
% identity	62
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]
Seq. No.	30521
Contig ID	216137_1.R1040
5'-most EST	zhf700955669.h1
Method	BLASTN
NCBI GI	g1239962
BLAST score	38
E value	4.0e-12
Match length	62
% identity	90
NCBI Description	A.majus mRNA for MADS-box protein (DEFH72)
Seq. No.	30522
Contig ID	216144_1.R1040
5'-most EST	zhf700955668.h1
Seq. No.	30523
Contig ID	216209_1.R1040
5'-most EST	zsg701119566.h1
Method	BLASTX
NCBI GI	g3256848
BLAST score	175
E value	8.0e-13
Match length	100
% identity	40
NCBI Description	(AP000002) 219aa long hypothetical protein [Pyrococcus horikoshii]

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Seq. No.          30554
Contig ID         216958_1.R1040
5'-most EST      uC-gmflminsoy016d12b1
Method            BLASTX
NCBI GI           g4336426
BLAST score       548
E value           2.0e-56
Match length      127
% identity        77
NCBI Description  (AF090835) Ca2+-dependen
                  crystallinum]
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Seq. No.	30557
Contig ID	217019_1.R1040
5'-most EST	zhf700956924.h1

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Seq. No.          30561
Contig ID         217082_1.R1040
5'-most EST      zhf700957045.h1
Method            BLASTX
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Seq. No.	30607
Contig ID	218067_1.R1040
5'-most EST	fua701042740.h1

Seq. No.	30608
Contig ID	218077_1.R1040
5'-most EST	zhf700958626.h1

Seq. No.	30609
Contig ID	218084_1.R1040
5'-most EST	zhf700958634.h1

Seq. No.	30610
Contig ID	218112_1.R1040
5'-most EST	zhf700959017.h1

Seq. No.	30611
Contig ID	218118_1.R1040
5'-most EST	zhf700958705.h1

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Seq. No.          30612
Contig ID         218163_1.R1040
5'-most EST ----- jC-gmf102220114g03d1
```

Seq. No.	30613
Contig ID	218232_1.R1040
5'-most EST	zhf700958874.h1

```
Seq. No.          30614
Contig ID         218272_1.R1040
5'-most EST      zhf700958932.h1
Method            BLASTX
NCBI GI           g4371293
BLAST score       162
E value           4.0e-11
Match length      132
% identity        34
NCBI Description  (AC006260) hypothetical protein [Arabidopsis thaliana]
```

Seq. No.	30615
Contig ID	218304_1.R1040
5'-most EST	qsv701055031.h1

```
Seq. No.          30616
Contig ID         218350_1.R1040
5'-most EST      zhf700959050.h1
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Seq. No.	30617
Contig ID	218384_1.R1040
5'-most EST	asn701138736.h1

```
Seq. No.          30618
Contig ID         218391_1.R1040
5'-most EST      kl1701208301.h1
Method            BLASTX
NCBI GI           q4098647
```


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BLAST score 248
 E value 2.0e-21
 Match length 107
 % identity 47
 NCBI Description (U28742) highly similar to alpha-adaptin (rat and mouse)
 [Caenorhabditis elegans]

Seq. No. 30706
 Contig ID 220765_1.R1040
 5'-most EST dpv701096980.h1

Seq. No. 30707
 Contig ID 220766_1.R1040
 5'-most EST epx701110249.h1

Seq. No. 30708
 Contig ID 220819_1.R1040
 5'-most EST jC-gmst02400015h12a1

Seq. No. 30709
 Contig ID 220859_1.R1040
 5'-most EST gsv701045933.h1

Seq. No. 30710
 Contig ID 220860_1.R1040
 5'-most EST zhf700962718.h1

Seq. No. 30711
 Contig ID 220918_1.R1040
 5'-most EST zhf700962796.h1

Seq. No. 30712
 Contig ID 220919_1.R1040
 5'-most EST zhf700962801.h1
 Method BLASTX
 NCBI GI g3135274
 BLAST score 169
 E value 3.0e-12
 Match length 48
 % identity 65
 NCBI Description (AC003058) putative beta-1,3-endoglucanase [Arabidopsis
 thaliana]

Seq. No. 30713
 Contig ID 220930_1.R1040
 5'-most EST asn701138573.h1
 Method BLASTX
 NCBI GI g1881268
 BLAST score 190
 E value 2.0e-14
 Match length 104
 % identity 40
 NCBI Description (AB001488) ATP-DEPENDENT RNA HELICASE DEAD HOMOLOG.
 [Bacillus subtilis] >gi_2632758_emb_CAB12265_(Z99106)
 similar to ATP-dependent RNA helicase [Bacillus subtilis]

Seq. No. 30714

Seq. No. 30735
 Contig ID 221576 1.R1040
 5'-most EST g5606666
 Method BLASTX
 NCBI GI g3004564
 BLAST score 193
 E value 1.0e-14
 Match length 79
 % identity 52
 NCBI Description (AC003673) putative receptor Ser/Thr protein kinase
 [Arabidopsis thaliana]

Seq. No. 30736
 Contig ID 221590 1.R1040
 5'-most EST epX701106304.h1
 Method BLASTX
 NCBI GI g3269289
 BLAST score 152
 E value 4.0e-10
 Match length 50
 % identity 64
 NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 30737
 Contig ID 221624 1.R1040
 5'-most EST jC-gmfl02220084f12a1
 Method BLASTX
 NCBI GI g2842496
 BLAST score 147
 E value 2.0e-09
 Match length 32
 % identity 81
 NCBI Description (AL021749) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No. 30738
 Contig ID 221631 1.R1040
 5'-most EST zhf700964218.h1
 Method BLASTX
 NCBI GI g2979544
 BLAST score 238
 E value 7.0e-20
 Match length 96
 % identity 47
 NCBI Description (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No. 30739
 Contig ID 221687 1.R1040
 5'-most EST zhf700963743.h1

Seq. No. 30740
 Contig ID 221730 1.R1040
 5'-most EST zhf700963803.h1
 Method BLASTX
 NCBI GI g4220461
 BLAST score 169
 E value 9.0e-12

Match length	114
% identity	37
NCBI Description	(AC006216) ESTs gb_T75642 and gb_AA650997 come from this gene. [Arabidopsis thaliana]
Seq. No.	30741
Contig ID	221741_1.R1040
5'-most EST	leu701156407.h1
Seq. No.	30742
Contig ID	221754_1.R1040
5'-most EST	uC-gmrominsoy061f11b1
Method	BLASTN
NCBI GI	g556421
BLAST score	53
E value	6.0e-21
Match length	113
% identity	87
NCBI Description	Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1) mRNA, complete cds
Seq. No.	30743
Contig ID	221773_1.R1040
5'-most EST	jC-gmle01810084d05a1
Method	BLASTX
NCBI GI	g4249412
BLAST score	582
E value	3.0e-60
Match length	146
% identity	76
NCBI Description	(AC006072) hypothetical protein [Arabidopsis thaliana]
Seq. No.	30744
Contig ID	221801_1.R1040
5'-most EST	zhf700963882.h1
Method	BLASTX
NCBI GI	g2252836
BLAST score	355
E value	5.0e-34
Match length	95
% identity	77
NCBI Description	(AF013293) contains weak similarity to S. cerevisiae BOB1 protein (PIR:S45444) [Arabidopsis thaliana]
Seq. No.	30745
Contig ID	221828_1.R1040
5'-most EST	zhf700963921.h1
Method	BLASTX
NCBI GI	g4206209
BLAST score	320
E value	5.0e-30
Match length	74
% identity	80
NCBI Description	(AF071527) putative glucan synthase component [Arabidopsis thaliana] >gi_4263042_gb_AAD15311_(AC005142) putative glucan synthase component [Arabidopsis thaliana]

Match length 86
 % identity 64
 NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 30754
 Contig ID 222071_1.R1040
 5'-most EST uC-gmrñnoir030d08b1

Seq. No. 30755
 Contig ID 222081_1.R1040
 5'-most EST zhf700964239.h1

Seq. No. 30756
 Contig ID 222132_1.R1040
 5'-most EST jC-gmfl02220108d01d1

Seq. No. 30757
 Contig ID 222148_1.R1040
 5'-most EST zhf700964326.h1
 Method BLASTX
 NCBI GI g2108252
 BLAST score 343
 E value 2.0e-32
 Match length 123
 % identity 25
 NCBI Description (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
 >gi_2108254_emb_CAA71276_(Y10227) P-glycoprotein-2
 [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1
 (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No. 30758
 Contig ID 222167_1.R1040
 5'-most EST fua701040929.h1

Seq. No. 30759
 Contig ID 222211_1.R1040
 5'-most EST zhf700964402.h1

Seq. No. 30760
 Contig ID 222220_1.R1040
 5'-most EST zsg701127981.h1
 Method BLASTX
 NCBI GI g629602
 BLAST score 476
 E value 5.0e-92
 Match length 302
 % identity 58
 NCBI Description probable imbibition protein - wild cabbage
 >gi_488787_emb_CAA55893_(X79330) putative imbibition
 protein [Brassica oleracea]

Seq. No. 30761
 Contig ID 222252_1.R1040
 5'-most EST zhf700964451.h1

Seq. No. 30762
 Contig ID 222263_1.R1040

5'-most EST zhf700964464.h1

Seq. No. 30763
Contig ID 222273_1.R1040
5'-most EST zsg701123360.h1

Seq. No. 30764
Contig ID 222292_1.R1040
5'-most EST zhf700964501.h1
Method BLASTX
NCBI GI g3540181
BLAST score 561
E value 7.0e-76
Match length 203
% identity 70
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 30765
Contig ID 222300_1.R1040
5'-most EST uC-gmropic104h05b1
Method BLASTN
NCBI GI g2330650
BLAST score 141
E value 2.0e-73
Match length 377
% identity 84
NCBI Description Pisum sativum mRNA for topoisomerase II

Seq. No. 30766
Contig ID 222338_1.R1040
5'-most EST zhf700964559.h1
Method BLASTN
NCBI GI g3786500
BLAST score 33
E value 4.0e-09
Match length 59
% identity 3
NCBI Description Caenorhabditis elegans cosmid T06A4

Seq. No. 30767
Contig ID 222412_1.R1040
5'-most EST zhf700964650.h1
Method BLASTX
NCBI GI g2642448
BLAST score 161
E value 6.0e-11
Match length 131
% identity 12
NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]
>gi_3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30768
Contig ID 222417_1.R1040
5'-most EST zhf700964656.h1

Seq. No. 30769

Contig ID 222493_1.R1040
 5'-most EST asj700967309.h1
 Method BLASTX
 NCBI GI g728868
 BLAST score 197
 E value 2.0e-15
 Match length 52
 % identity 69
 NCBI Description ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
 >gi_99824_pir_S16748 proline-rich protein - rape
 (fragment) >gi_22597_emb_CAA42924_ (X60376) proline-rich
 protein [Brassica napus]

Seq. No. 30770
 Contig ID 222514_1.R1040
 5'-most EST zhf700964776.h1
 Method BLASTX
 NCBI GI g2921340
 BLAST score 668
 E value 7.0e-70
 Match length 201
 % identity 66
 NCBI Description (AF034134) MYB-like DNA-binding domain protein [Gossypium
 hirsutum]

Seq. No. 30771
 Contig ID 222527_1.R1040
 5'-most EST leu701156718.h1

Seq. No. 30772
 Contig ID 222546_1.R1040
 5'-most EST zhf700964815.h1
 Method BLASTX
 NCBI GI g3811347
 BLAST score 163
 E value 1.0e-11
 Match length 62
 % identity 47
 NCBI Description (AF065215) cytosolic phospholipase A2 beta [Homo sapiens]

Seq. No. 30773
 Contig ID 222548_1.R1040
 5'-most EST jC-gmle01810082b01a1
 Method BLASTX
 NCBI GI g3337366
 BLAST score 339
 E value 1.0e-31
 Match length 122
 % identity 26
 NCBI Description (AC004481) unknown protein [Arabidopsis thaliana]

Seq. No. 30774
 Contig ID 222569_1.R1040
 5'-most EST jC-gmfl02220060c12d1
 Method BLASTX
 NCBI GI g960289
 BLAST score 415

[illegible]

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Seq. No.          30801
Contig ID         223520_1.R1040
5'-most EST      crh700850473.h1
Method            BLASTX
NCBI GI           g2160163
BLAST score       270
E value           5.0e-24
Match length      70
% identity        45
NCBI Description  (AC000132) No definition line found [Arabidopsis thaliana]
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Seq. No.          30803
Contig ID         223620_1.R1040
5'-most EST      crh700850690.h1
Method            BLASTN
NCBI GI           g4220643
BLAST score       35
E value           4.0e-10
Match length      51
% identity        92
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Seq. No.	30804
Contig ID	223624.1.R1040
5'-most EST	jC-qmr002910062f05a1

Seq. No.	30805
Contig ID	223633_1.R1040
5'-most EST	zsq701124347.h1

4720

% identity	64
NCBI Description	(AC006068) putative receptor protein kinase [Arabidopsis thaliana]
Seq. No.	30835
Contig ID	224708_1.R1040
5'-most EST	epx701109365.h1
Seq. No.	30836
Contig ID	224713_1.R1040
5'-most EST	fC-gmse700852469f1
Method	BLASTX
NCBI GI	g2497752
BLAST score	320
E value	1.0e-29
Match length	116
% identity	53
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1321911_emb_CAA65475_ (X96714) lipid transfer protein [Prunus dulcis]
Seq. No.	30837
Contig ID	224742_1.R1040
5'-most EST	rlr700901185.h1
Seq. No.	30838
Contig ID	224744_1.R1040
5'-most EST	uC-gmröpic016a07b1
Seq. No.	30839
Contig ID	224806_1.R1040
5'-most EST	crh700852610.h1
Seq. No.	30840
Contig ID	224846_1.R1040
5'-most EST	fC-gmrö700844279d3
Seq. No.	30841
Contig ID	224900_1.R1040
5'-most EST	leu701155145.h1
Method	BLASTX
NCBI GI	g3080375
BLAST score	496
E value	3.0e-50
Match length	124
% identity	75
NCBI Description	(AL022580) putative protein [Arabidopsis thaliana]
Seq. No.	30842
Contig ID	224907_1.R1040
5'-most EST	crh700852746.h1
Seq. No.	30843
Contig ID	224964_1.R1040
5'-most EST	fC-gmse700839629g1
Seq. No.	30844

[illegible]

Contig ID 227026 1.R1040
5'-most EST pmv700892102.h1

Seq. No. 30903
Contig ID 227040 2.R1040
5'-most EST pmv700888509.h1

Seq. No. 30904
Contig ID 227045 1.R1040
5'-most EST pmv700888414.h1

Seq. No. 30905
Contig ID 227057 1.R1040
5'-most EST g4284686
Method BLASTX
NCBI GI g1755192
BLAST score 201
E value 5.0e-26
Match length 95
% identity 66
NCBI Description (U75207) germin-like protein [Arabidopsis thaliana]

Seq. No. 30906
Contig ID 227060 1.R1040
5'-most EST uC-gmropic018d03b1

Seq. No. 30907
Contig ID 227081 1.R1040
5'-most EST jsh701069769.h1
Method BLASTX
NCBI GI g1703376
BLAST score 297
E value 3.0e-27
Match length 67
% identity 85
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_480121_pir_S36453
ADP-ribosylation factor 1 - potato >gi_396808_emb_CAA52468_
(X74461) ADP-ribosylation factor 1 [Solanum tuberosum]

Seq. No. 30908
Contig ID 227097 1.R1040
5'-most EST pmv700888489.h1

Seq. No. 30909
Contig ID 227101 1.R1040
5'-most EST pmv700888494.h1
Method BLASTN
NCBI GI g429107
BLAST score 100
E value 4.0e-49
Match length 248
% identity 85
NCBI Description L.esculentum S-adenosyl-L-methionine synthetase mRNA,
complete CDS

Seq. No. 30910
Contig ID 227192 1.R1040

5'-most EST	jC-gmf102220089a09d1
Seq. No.	30911
Contig ID	227194_1.R1040
5'-most EST	leu701155561.h1
Seq. No.	30912
Contig ID	227202_1.R1040
5'-most EST	jC-gmst02400034g02d2
Seq. No.	30913
Contig ID	227289_1.R1040
5'-most EST	pmv700888746.h1
Seq. No.	30914
Contig ID	227328_1.R1040
5'-most EST	pmv700888821.h1
Method	BLASTX
NCBI GI	g4249411
BLAST score	210
E value	1.0e-16
Match length	42
% identity	93
NCBI Description	(AC006072) unknown protein [Arabidopsis thaliana]
Seq. No.	30915
Contig ID	227329_1.R1040
5'-most EST	pmv700888822.h1
Seq. No.	30916
Contig ID	227360_1.R1040
5'-most EST	leu701154547.h1
Seq. No.	30917
Contig ID	227369_1.R1040
5'-most EST	uC-gmröpic007h11b1
Method	BLASTX
NCBI GI	g1076315
BLAST score	172
E value	3.0e-12
Match length	101
% identity	40
NCBI Description	cytochrome P450 - Arabidopsis thaliana >gi_853719_emb_CAA60793_(X87367) CYP90 protein [Arabidopsis thaliana] >gi_871988_emb_CAA60794_(X87368) CYP90 protein [Arabidopsis thaliana]
Seq. No.	30918
Contig ID	227373_1.R1040
5'-most EST	pmv700888873.h1
Seq. No.	30919
Contig ID	227387_1.R1040
5'-most EST	rlr700896045.h1
Seq. No.	30920
Contig ID	227421_1.R1040

E value 7.0e-14
 Match length 89
 % identity 47
 NCBI Description TRANSCRIPTION FACTOR E2F5 (E2F-5) >gi_2137276_pir_I48338
 E2F-5 - mouse >gi_806572_emb_CAA60508_ (X86925) E2F-5 [Mus
 musculus]

Seq. No. 30926
 Contig ID 227471_1.R1040
 5'-most EST pxt700944495.h1

Seq. No. 30927
 Contig ID 227472_1.R1040
 5'-most EST pmv700888994.h1

Seq. No. 30928
 Contig ID 227528_1.R1040
 5'-most EST pxt700942665.h1
 Method BLASTX
 NCBI GI g1420936
 BLAST score 1002
 E value 1.0e-109
 Match length 237
 % identity 76
 NCBI Description (U61396) Vigna unguiculata aspartic proteinase mRNA,
 complete cds. [Vigna unguiculata]

Seq. No. 30929
 Contig ID 227532_1.R1040
 5'-most EST asn701134848.h2
 Method BLASTX
 NCBI GI g3386605
 BLAST score 168
 E value 5.0e-22
 Match length 86
 % identity 57
 NCBI Description (AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30930
 Contig ID 227551_1.R1040
 5'-most EST pmv700889088.h1

Seq. No. 30931
 Contig ID 227554_1.R1040
 5'-most EST pxt700941410.h1

Seq. No. 30932
 Contig ID 227589_1.R1040
 5'-most EST jC-gmle01810049a08d1

Seq. No. 30933
 Contig ID 227602_1.R1040
 5'-most EST pmv700889151.h1
 Method BLASTX
 NCBI GI g1742955
 BLAST score 667
 E value 4.0e-70

E value 4.0e-22
 Match length 69
 % identity 32
 NCBI Description (AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30942
 Contig ID 227769_1.R1040
 5'-most EST pmv700889360.h1
 Method BLASTX
 NCBI GI g3258569
 BLAST score 465
 E value 1.0e-46
 Match length 121
 % identity 79
 NCBI Description (U89959) Similar to yeast general negative regulator of transcription subunit 1 [Arabidopsis thaliana]

Seq. No. 30943
 Contig ID 227797_1.R1040
 5'-most EST pmv700889393.h1
 Method BLASTX
 NCBI GI g3327271
 BLAST score 231
 E value 3.0e-19
 Match length 100
 % identity 52
 NCBI Description (AB016000) PKn2 [Ipomoea nil]

Seq. No. 30944
 Contig ID 227918_1.R1040
 5'-most EST g4300792

Seq. No. 30945
 Contig ID 227960_1.R1040
 5'-most EST jC-gmro02910047b01a1
 Method BLASTX
 NCBI GI g4490300
 BLAST score 430
 E value 2.0e-42
 Match length 121
 % identity 73
 NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 30946
 Contig ID 227989_1.R1040
 5'-most EST pxt700940986.h1
 Method BLASTX
 NCBI GI g1360090
 BLAST score 300
 E value 2.0e-27
 Match length 106
 % identity 60
 NCBI Description (X95576) ClC-Nt1 [Nicotiana tabacum]

Seq. No. 30947
 Contig ID 228004_1.R1040
 5'-most EST leu701154017.h1

Seq. No. 30948
 Contig ID 228031_1.R1040
 5'-most EST fC-gmro700870127f3
 Method BLASTX
 NCBI GI g3269291
 BLAST score 417
 E value 8.0e-41
 Match length 181
 % identity 49
 NCBI Description (AL030978) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 30949
 Contig ID 228040_1.R1040
 5'-most EST gsv701054529.h1

Seq. No. 30950
 Contig ID 228042_1.R1040
 5'-most EST fC-gmro700870195a4
 Method BLASTX
 NCBI GI g2853078
 BLAST score 147
 E value 4.0e-09
 Match length 161
 % identity 19
 NCBI Description (AL021768) TMV resistance protein N-like [Arabidopsis thaliana]

Seq. No. 30951
 Contig ID 228046_1.R1040
 5'-most EST pmv700889742.h1
 Method BLASTX
 NCBI GI g2914698
 BLAST score 388
 E value 8.0e-40
 Match length 190
 % identity 45
 NCBI Description (AC003974) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30952
 Contig ID 228054_1.R1040
 5'-most EST dkc700968025.h1

Seq. No. 30953
 Contig ID 228054_2.R1040
 5'-most EST jsh701064341.h1

Seq. No. 30954
 Contig ID 228054_3.R1040
 5'-most EST pxt700942158.h1

Seq. No. 30955
 Contig ID 228064_1.R1040
 5'-most EST hrw701063230.h1

Seq. No. 30956

09684015_101000

Contig ID	228066_1.R1040
5'-most EST	pmv700889774.h1
Seq. No.	30957
Contig ID	228121_1.R1040
5'-most EST	epx701106844.h1
Method	BLASTX
NCBI GI	g3695019
BLAST score	287
E value	6.0e-26
Match length	97
% identity	57
NCBI Description	(AF055848) subtilisin-like protease [Arabidopsis thaliana]
Seq. No.	30958
Contig ID	228141_1.R1040
5'-most EST	jC-gmle01810063e05a1
Seq. No.	30959
Contig ID	228145_1.R1040
5'-most EST	fC-gmle700870650f3
Method	BLASTX
NCBI GI	g2129698
BLAST score	669
E value	2.0e-93
Match length	219
% identity	79
NCBI Description	protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana >gi_1054633_emb_CAA63387_ (X92728) protein kinase [Arabidopsis thaliana]
Seq. No.	30960
Contig ID	228152_1.R1040
5'-most EST	jC-gmst02400005g06a1
Seq. No.	30961
Contig ID	228155_1.R1040
5'-most EST	jC-gmro02910004e07a1
Seq. No.	30962
Contig ID	228157_1.R1040
5'-most EST	pmv700889894.h1
Method	BLASTX
NCBI GI	g3935181
BLAST score	184
E value	4.0e-20
Match length	60
% identity	83
NCBI Description	(AC004557) F17L21.24 [Arabidopsis thaliana]
Seq. No.	30963
Contig ID	228167_1.R1040
5'-most EST	pmv700889912.h1
Method	BLASTX
NCBI GI	g2832661
BLAST score	323
E value	4.0e-30

5'-most EST uC-gmrominsoy277g05b1
Method BLASTX
NCBI GI g4218120
BLAST score 231
E value 5.0e-19
Match length 144
% identity 35
NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No. 30972
Contig ID 228398_1.R1040
5'-most EST jC-gmst02400044f01a1
Method BLASTX
NCBI GI g1350783
BLAST score 667
E value 8.0e-70
Match length 321
% identity 48
NCBI Description RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR
>gi_282883_pir_S27756 receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166850 (M84660) receptor-like protein kinase [Arabidopsis thaliana]
>gi_2842492_emb_CAA16889_ (AL021749) receptor-like protein kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. No. 30973
Contig ID 228435_1.R1040
5'-most EST fC-gmle700871051f3
Method BLASTX
NCBI GI g4539383
BLAST score 379
E value 9.0e-37
Match length 93
% identity 76
NCBI Description (AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No. 30974
Contig ID 228442_1.R1040
5'-most EST jC-gmst02400047d09a1

Seq. No. 30975
Contig ID 228471_1.R1040
5'-most EST pmv700892204.h1

Seq. No. 30976
Contig ID 228489_1.R1040
5'-most EST pmv700892264.h1
Method BLASTX
NCBI GI g4115563
BLAST score 268
E value 2.0e-26
Match length 82
% identity 71
NCBI Description (AB013598) UDP-glucose:anthocyanin 5-O-glucosyltransferase [Verbena x hybrida]

NCBI Description finger protein pcpl - potato >gi_563623_emb_CAA57772_ (X82328) putative DNA/RNA binding protein [Solanum tuberosum]

Seq. No. 30993
Contig ID 229088_1.R1040
5'-most EST fC-gmro7000749140r1

Seq. No. 30994
Contig ID 229101_1.R1040
5'-most EST pmv700891126.h1

Seq. No. 30995
Contig ID 229117_1.R1040
5'-most EST uC-gmropic025h05b1
Method BLASTX
NCBI GI g2104534
BLAST score 596
E value 5.0e-62
Match length 129
% identity 84
NCBI Description (AF001308) hypothetical protein [Arabidopsis thaliana]

Seq. No. 30996
Contig ID 229131_1.R1040
5'-most EST kl1701213809.h1

Seq. No. 30997
Contig ID 229150_1.R1040
5'-most EST zsg701124540.h1
Method BLASTX
NCBI GI g3880026
BLAST score 277
E value 1.0e-25
Match length 101
% identity 55
NCBI Description (Z75550) Similarity with Schizosaccharomyces hypothetical gene (TREMBL ID G847708); cDNA EST EMBL:M89418 comes from this gene [Caenorhabditis elegans]

Seq. No. 30998
Contig ID 229155_1.R1040
5'-most EST asn701133270.h1
Method BLASTX
NCBI GI g3763933
BLAST score 715
E value 1.0e-75
Match length 187
% identity 85
NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]

Seq. No. 30999
Contig ID 229165_1.R1040
5'-most EST pmv700891209.h1

Seq. No. 31000
Contig ID 229271_1.R1040


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5'-most EST      dpv701100873.h1
Method           BLASTX
NCBI GI          g4115384
BLAST score      459
E value          4.0e-46
Match length     106
% identity       79
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.         31008
Contig ID        229445_1.R1040
5'-most EST      pmv700891569.h1
Method           BLASTX
NCBI GI          g3786021
BLAST score      191
E value          1.0e-14
Match length     66
% identity       58
NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No.         31009
Contig ID        229465_1.R1040
5'-most EST      fC-gmle700872274f7
Method           BLASTX
NCBI GI          g2760839
BLAST score      756
E value          4.0e-86
Match length     252
% identity       67
NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.         31010
Contig ID        229503_1.R1040
5'-most EST      jC-gmst02400001b07a1
Method           BLASTX
NCBI GI          g2827143
BLAST score      286
E value          6.0e-26
Match length     64
% identity       72
NCBI Description (AF027174) cellulose synthase catalytic subunit
[Arabidopsis thaliana]

Seq. No.         31011
Contig ID        229607_1.R1040
5'-most EST      jC-gmro02910024g02d1

Seq. No.         31012
Contig ID        229643_1.R1040
5'-most EST      jC-gmro02910048b02a1
Method           BLASTX
NCBI GI          g3360289
BLAST score      164
E value          3.0e-11
Match length     54
% identity       54
NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase

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0503416-1000

Seq. No.	31014
Contig ID	229658_1.R1040
5'-most EST	fC-gmle700873056f3
Method	BLASTX
NCBI GI	g2795809
BLAST score	319
E value	3.0e-29
Match length	64
% identity	88
NCBI Description	(AC003674) putativ

```
Seq. No.          31016
Contig ID         229704_1.R1040
5'-most EST      pmv700891910.h1
Method            BLASTN
NCBI GI           g1850545
BLAST score       34
E value           2.0e-09
Match length      115
% identity        89
NCBI Description  Arabidopsis thaliana syntaxin related protein AtVam3p
                  (AtVAM3) mRNA, complete cds
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```
Seq. No.          31017
Contig ID         229839_1.R1040
5'-most EST      fC-gmle700873194f3
Method           BLASTX
NCBI GI          g1350783
BLAST score       400
E value          6.0e-39
Match length      149
% identity        9
NCBI Description  RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR
                  >gi_282883_pir_S27756 receptor-like protein kinase
                  precursor - Arabidopsis thaliana >gi_166850 (M84660)
                  receptor-like protein kinase [Arabidopsis thaliana]
                  >gi_2842492_emb_CAA16889 (AL021749) receptor-like protein
                  kinase 5 precursor (RLK5) [Arabidopsis thaliana]
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Contig ID 230253_2.R1040
 5'-most EST jC-gmst02400020c12a1
 Method BLASTX
 NCBI GI g3757521
 BLAST score 268
 E value 2.0e-23
 Match length 98
 % identity 52
 NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 31039
 Contig ID 230258_1.R1040
 5'-most EST pmv700892661.h1

Seq. No. 31040
 Contig ID 230264_1.R1040
 5'-most EST pmv700892668.h1
 Method BLASTX
 NCBI GI g1730133
 BLAST score 158
 E value 4.0e-10
 Match length 87
 % identity 38
 NCBI Description ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE
 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV)
 (ELAM-1 LIGAND FUCOSYLTRANSFERASE) >gi_105261_pir_A40976
 alpha(1,3)-fucosyltransferase (EC 2.4.1.-) - human
 >gi_1236720 (M65030) alpha(1,3)-fucosyltransferase [Homo
 sapiens]

Seq. No. 31041
 Contig ID 230319_1.R1040
 5'-most EST pmv700892794.h1

Seq. No. 31042
 Contig ID 230343_2.R1040
 5'-most EST gsv701048887.h1

Seq. No. 31043
 Contig ID 230382_1.R1040
 5'-most EST pmv700892877.h1
 Method BLASTX
 NCBI GI g3434969
 BLAST score 168
 E value 2.0e-11
 Match length 107
 % identity 44
 NCBI Description (AB008104) ethylene responsive element binding factor 2
 [Arabidopsis thaliana]

Seq. No. 31044
 Contig ID 230410_1.R1040
 5'-most EST pmv700892924.h1
 Method BLASTX
 NCBI GI g2191193
 BLAST score 183
 E value 2.0e-13

Match length 153
 % identity 29
 NCBI Description (AF007271) contain similarity to type 1 inositol
 1,4,5-triphosphate receptors [Arabidopsis thaliana]

Seq. No. 31045
 Contig ID 230429_2.R1040
 5'-most EST jC-gmfl02220131e01d1
 Method BLASTX
 NCBI GI g4006831
 BLAST score 165
 E value 3.0e-11
 Match length 82
 % identity 43
 NCBI Description (AC005970) putative reverse transcriptase [Arabidopsis
 thaliana]

Seq. No. 31046
 Contig ID 230430_1.R1040
 5'-most EST fC-gmle700877271f1
 Method BLASTX
 NCBI GI g2961358
 BLAST score 231
 E value 3.0e-19
 Match length 105
 % identity 48
 NCBI Description (AL022140) serine/threonine protein kinase like protein
 [Arabidopsis thaliana]

Seq. No. 31047
 Contig ID 230467_1.R1040
 5'-most EST pmv700894827.h1

Seq. No. 31048
 Contig ID 230484_1.R1040
 5'-most EST gsv701048525.h1

Seq. No. 31049
 Contig ID 230496_1.R1040
 5'-most EST leu701148894.h1
 Method BLASTX
 NCBI GI g2160694
 BLAST score 666
 E value 3.0e-70
 Match length 138
 % identity 90
 NCBI Description (U73528) B' regulatory subunit of PP2A [Arabidopsis
 thaliana]

Seq. No. 31050
 Contig ID 230500_1.R1040
 5'-most EST asn701141708.h1

Seq. No. 31051
 Contig ID 230507_1.R1040
 5'-most EST pmv700893055.h1
 Method BLASTX

NCBI GI g2618698
 BLAST score 324
 E value 4.0e-32
 Match length 104
 % identity 61
 NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 31052
 Contig ID 230521_1.R1040
 5'-most EST pmv700893071.h1

Seq. No. 31053
 Contig ID 230522_1.R1040
 5'-most EST pmv700893072.h1

Seq. No. 31054
 Contig ID 230527_1.R1040
 5'-most EST pmv700893083.h1

Seq. No. 31055
 Contig ID 230545_1.R1040
 5'-most EST pmv700893117.h1
 Method BLASTX
 NCBI GI g3334200
 BLAST score 390
 E value 4.0e-38
 Match length 94
 % identity 80
 NCBI Description GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)
 >gi_2894362_emb_CAB16918_ (Z99770) P-Protein precursor
 [Solanum tuberosum]

Seq. No. 31056
 Contig ID 230550_1.R1040
 5'-most EST zsg701122283.h1

Seq. No. 31057
 Contig ID 230635_1.R1040
 5'-most EST rlr700896343.h1

Seq. No. 31058
 Contig ID 230690_1.R1040
 5'-most EST g4282637
 Method BLASTX
 NCBI GI g1346792
 BLAST score 186
 E value 7.0e-14
 Match length 119
 % identity 36
 NCBI Description DNA PRIMASE SMALL SUBUNIT (DNA PRIMASE 49 KD SUBUNIT) (P49)
 >gi_631124_pir_S45630 DNA primase chain p48 - human
 >gi_510406_emb_CAA52377_ (X74330) DNA primase (subunit p48)
 [Homo sapiens] >gi_4506051_ref_NP_000937.1_pPRIM1_ primase,
 polypeptide 1 (49kD)

Seq. No. 31059

NCBI Description Vigna radiata carboxypeptidase II mRNA, partial cds

Seq. No. 31098
 Contig ID 231856_1.R1040
 5'-most EST pmv700894885.h1
 Method BLASTX
 NCBI GI g4455284
 BLAST score 410
 E value 4.0e-40
 Match length 112
 % identity 69
 NCBI Description (AL035527) beta-glucosidase-like protein [Arabidopsis thaliana]

Seq. No. 31099
 Contig ID 231857_1.R1040
 5'-most EST uC-gmrominsoy229c05b1

Seq. No. 31100
 Contig ID 231881_1.R1040
 5'-most EST pmv700894927.h1

Seq. No. 31101
 Contig ID 231887_1.R1040
 5'-most EST pmv700894938.h1

Seq. No. 31102
 Contig ID 231981_1.R1040
 5'-most EST pmv700895087.h1
 Method BLASTN
 NCBI GI g22738
 BLAST score 147
 E value 4.0e-77
 Match length 259
 % identity 94
 NCBI Description G.max mitochondrial atpA

Seq. No. 31103
 Contig ID 231984_1.R1040
 5'-most EST pmv700895091.h1

Seq. No. 31104
 Contig ID 232044_1.R1040
 5'-most EST pmv700895173.h1
 Method BLASTX
 NCBI GI g2160156
 BLAST score 578
 E value 8.0e-60
 Match length 145
 % identity 76
 NCBI Description (AC000132) Strong similarity to S. pombe leucyl-tRNA synthetase (gb_Z73100). [Arabidopsis thaliana]

Seq. No. 31105
 Contig ID 232062_1.R1040
 5'-most EST pmv700895196.h1
 Method BLASTX

Match length 171
 % identity 82
 NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No. 31112
 Contig ID 232321_1.R1040
 5'-most EST g4313762
 Method BLASTX
 NCBI GI g2460200
 BLAST score 375
 E value 8.0e-36
 Match length 147
 % identity 54
 NCBI Description (AF020833) eukaryotic translation initiation factor 3 subunit [Homo sapiens]

Seq. No. 31113
 Contig ID 232321_2.R1040
 5'-most EST uC-gmrominsoyl80f04b1

Seq. No. 31114
 Contig ID 232377_1.R1040
 5'-most EST uC-gmropic058d02b1
 Method BLASTX
 NCBI GI g2501011
 BLAST score 495
 E value 5.0e-50
 Match length 159
 % identity 56
 NCBI Description ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS)
 >gi_1652625_dbj_BAA17545_(D90907) isoleucyl-tRNA
 synthetase [Synecocystis sp.]

Seq. No. 31115
 Contig ID 232381_1.R1040
 5'-most EST pxt700941004.h1

Seq. No. 31116
 Contig ID 232394_1.R1040
 5'-most EST uC-gmronoir043h04b1
 Method BLASTX
 NCBI GI g1407705
 BLAST score 721
 E value 2.0e-76
 Match length 158
 % identity 79
 NCBI Description (U60202) lipoxygenase [Solanum tuberosum]

Seq. No. 31117
 Contig ID 232397_1.R1040
 5'-most EST zsg701122060.h1

Seq. No. 31118
 Contig ID 232422_1.R1040
 5'-most EST pxt700941055.h1
 Method BLASTX

NCBI GI g2501231
 BLAST score 392
 E value 2.0e-47
 Match length 118
 % identity 76
 NCBI Description HYPOTHETICAL 38.1 KD PROTEIN >gi_99505_pir_S24930
 hypothetical protein - pink corydalis
 >gi_18258_emb_CAA45139_(X63595) protein of unknown
 function [Corydalis sempervirens] >gi_444333_prf_1906382A
 pCSC71 protein [Corydalis sempervirens]

Seq. No. 31119
 Contig ID 232443_1.R1040
 5'-most EST jC-gmro02910006a02d1

Seq. No. 31120
 Contig ID 232474_1.R1040
 5'-most EST pxt700941117.h1
 Method BLASTX
 NCBI GI g4406819
 BLAST score 549
 E value 3.0e-56
 Match length 155
 % identity 72
 NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]

Seq. No. 31121
 Contig ID 232503_1.R1040
 5'-most EST pxt700941149.h1

Seq. No. 31122
 Contig ID 232518_1.R1040
 5'-most EST kl1701211586.h1

Seq. No. 31123
 Contig ID 232519_1.R1040
 5'-most EST leu701148185.h1
 Method BLASTN
 NCBI GI g3688527
 BLAST score 185
 E value 1.0e-99
 Match length 512
 % identity 84
 NCBI Description Pisum sativum mRNA for TPE4A thiol-protease

Seq. No. 31124
 Contig ID 232560_1.R1040
 5'-most EST zsg701128408.h1
 Method BLASTX
 NCBI GI g2285885
 BLAST score 327
 E value 9.0e-31
 Match length 90
 % identity 70
 NCBI Description (D89631) sulfate transporter [Arabidopsis thaliana]

Seq. No. 31125

5'-most EST leu701151322.h1
Method BLASTN
NCBI GI g3046856
BLAST score 37
E value 2.0e-11
Match length 45
% identity 96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No. 31169
Contig ID 233892_1.R1040
5'-most EST pxt700943588.h1

Seq. No. 31170
Contig ID 233947_1.R1040
5'-most EST pxt700943659.h1

Seq. No. 31171
Contig ID 233982_1.R1040
5'-most EST pxt700943708.h1
Method BLASTX
NCBI GI g2832300
BLAST score 430
E value 2.0e-42
Match length 114
% identity 70
NCBI Description (AF044285) adenosine-5'-phosphosulfate-kinase [Catharanthus roseus]

Seq. No. 31172
Contig ID 233985_1.R1040
5'-most EST pxt700943711.h1
Method BLASTX
NCBI GI g2194125
BLAST score 307
E value 4.0e-28
Match length 104
% identity 63
NCBI Description (AC002062) ESTs gb_R30459, gb_N38441 come from this gene. [Arabidopsis thaliana]

Seq. No. 31173
Contig ID 233992_1.R1040
5'-most EST pxt700943718.h1
Method BLASTX
NCBI GI g3885344
BLAST score 157
E value 9.0e-11
Match length 77
% identity 42
NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]
>gi_4557057_gb_AAD22497.1_AC007154_1 (AC007154) unknown protein [Arabidopsis thaliana]

Seq. No. 31174
Contig ID 234013_2.R1040

5'-most EST pxt700943740.h1

Seq. No. 31175
 Contig ID 234033_1.R1040
 5'-most EST pxt700943766.h1
 Method BLASTN
 NCBI GI g1816649
 BLAST score 322
 E value 0.0e+00
 Match length 437
 % identity 94
 NCBI Description *Lupinus luteus* NADH plastoquinone oxidoreductase subunit J (ndhJ) gene, chloroplast gene encoding chloroplast protein, complete cds

Seq. No. 31176
 Contig ID 234054_1.R1040
 5'-most EST gsv701053970.h1

Seq. No. 31177
 Contig ID 234083_1.R1040
 5'-most EST fua701038173.h1

Seq. No. 31178
 Contig ID 234101_1.R1040
 5'-most EST fC-gmst700652534d5
 Method BLASTN
 NCBI GI g294667
 BLAST score 47
 E value 3.0e-17
 Match length 59
 % identity 95
 NCBI Description *Castor bean* chloroplast beta-ketoacyl-ACP synthase (50 kDa synthase) mRNA, complete cds

Seq. No. 31179
 Contig ID 234102_1.R1040
 5'-most EST g4285233
 Method BLASTX
 NCBI GI g2130073
 BLAST score 269
 E value 8.0e-24
 Match length 60
 % identity 85
 NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [*Oryza sativa*] >gi_790970_dbj_BAA08830_ (D50301) aldolase C-1 [*Oryza sativa*]

Seq. No. 31180
 Contig ID 234107_1.R1040
 5'-most EST pxt700943860.h1

Seq. No. 31181
 Contig ID 234181_1.R1040
 5'-most EST jC-gmro02910056b03a1

Seq. No. 31213
 Contig ID 235182_1.R1040
 5'-most EST uC-gmrominsoy201a03b1
 Method BLASTX
 NCBI GI g4567311
 BLAST score 176
 E value 1.0e-12
 Match length 52
 % identity 63
 NCBI Description (AC005956) putative protein kinase [Arabidopsis thaliana]

Seq. No. 31214
 Contig ID 235238_1.R1040
 5'-most EST jC-gmfl02220073e02a1
 Method BLASTX
 NCBI GI g2827621
 BLAST score 411
 E value 5.0e-40
 Match length 207
 % identity 49
 NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 31215
 Contig ID 235281_1.R1040
 5'-most EST pxt700945368.h1
 Method BLASTN
 NCBI GI g1946219
 BLAST score 120
 E value 1.0e-60
 Match length 284
 % identity 86
 NCBI Description M.domestica mRNA for kn1-like protein (1791 bp)

Seq. No. 31216
 Contig ID 235318_1.R1040
 5'-most EST pxt700945415.h1

Seq. No. 31217
 Contig ID 235357_1.R1040
 5'-most EST uC-gmflminsoy025e06b1

Seq. No. 31218
 Contig ID 235369_1.R1040
 5'-most EST jC-gmle01810025a10a1

Seq. No. 31219
 Contig ID 235441_1.R1040
 5'-most EST jC-gmle01810005h06a1

Seq. No. 31220
 Contig ID 235573_1.R1040
 5'-most EST uC-gmropic103d04b1
 Method BLASTX
 NCBI GI g3608154
 BLAST score 334
 E value 3.0e-31

[Arabidopsis thaliana]

Seq. No. 31242
 Contig ID 236251_1.R1040
 5'-most EST uC-gmronoir006c12b1
 Method BLASTX
 NCBI GI g4454039
 BLAST score 247
 E value 5.0e-21
 Match length 151
 % identity 39
 NCBI Description (AL035394) putative Na⁺/H⁺-exchanging protein [Arabidopsis thaliana]

Seq. No. 31243
 Contig ID 236262_1.R1040
 5'-most EST uC-gmrominsoy207a08b1

Seq. No. 31244
 Contig ID 236269_1.R1040
 5'-most EST fC-gmf1700863687y1
 Method BLASTX
 NCBI GI g2494742
 BLAST score 775
 E value 1.0e-158
 Match length 334
 % identity 78
 NCBI Description GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE)
 >gi_2104791_emb_CAA73235_ (Y12704) glutamine synthetase
 [Agaricus bisporus]

Seq. No. 31245
 Contig ID 236290_1.R1040
 5'-most EST epX701104704.h1

Seq. No. 31246
 Contig ID 236341_1.R1040
 5'-most EST jC-gmro02910069g10d1

Seq. No. 31247
 Contig ID 236348_1.R1040
 5'-most EST asn701135735.h1

Seq. No. 31248
 Contig ID 236406_1.R1040
 5'-most EST g5057320
 Method BLASTX
 NCBI GI g4559340
 BLAST score 174
 E value 2.0e-12
 Match length 51
 % identity 76
 NCBI Description (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31249
 Contig ID 236412_1.R1040
 5'-most EST uC-gmrominsoy268h10b1

Seq. No. 31250
Contig ID 236477_1.R1040
5'-most EST rlr700895772.h1

Seq. No. 31251
Contig ID 236492_1.R1040
5'-most EST rlr700895654.h1
Method BLASTX
NCBI GI g1255448
BLAST score 316
E value 6.0e-29
Match length 90
% identity 71
NCBI Description (D50468) mitogen-activated protein kinase [Arabidopsis thaliana]

Seq. No. 31252
Contig ID 236524_1.R1040
5'-most EST asn701139977.h1
Method BLASTX
NCBI GI g2252840
BLAST score 308
E value 8.0e-36
Match length 158
% identity 47
NCBI Description (AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No. 31253
Contig ID 236544_1.R1040
5'-most EST rlr700895727.h1
Method BLASTX
NCBI GI g2462822
BLAST score 333
E value 5.0e-31
Match length 110
% identity 19
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31254
Contig ID 236620_1.R1040
5'-most EST rlr700895846.h1

Seq. No. 31255
Contig ID 236631_1.R1040
5'-most EST rlr700895865.h1
Method BLASTX
NCBI GI g4467359
BLAST score 182
E value 8.0e-14
Match length 82
% identity 11
NCBI Description (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis thaliana]

Seq. No. 31256

090761

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Seq. No.          31272
Contig ID         237426_1.R1040
5'-most EST      k11701202488.h1
Method            BLASTX
NCBI GI           g1814424
BLAST score       405
E value           1.0e-39
Match length      97
% identity        76
NCBI Description  (U85254) homeodomain protein AHDP [Arabidopsis thaliana]
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Seq. No.          31274
Contig ID         237506_1.R1040
5'-most EST      gsv701051920.h1
Method           BLASTX
NCBI GI          g3461836
BLAST score       379
E value          3.0e-36
Match length     189
% identity       42
NCBI Description  (AC005315) putative protein kinase [Arabidopsis thaliana]
                  >gi_3927841 (AC005727) putative protein kinase [Arabidopsis
                  thaliana]
```

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Seq. No.          31275
Contig ID         237520_1.R1040
5'-most EST      rlr700897244.h1
Method            BLASTX
NCBI GI           g2781359
BLAST score       162
E value           5.0e-16
Match length      105
% identity        54
NCBI Description  (AC003113) F2501.15 [Arabidopsis thaliana]
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E value	1.0e-10
Match length	50
% identity	51
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	31313
Contig ID	238987_1.R1040
5'-most EST	rlr700899662.h1
Seq. No.	31314
Contig ID	239004_1.R1040
5'-most EST	rlr700899684.h1
Seq. No.	31315
Contig ID	239066_1.R1040
5'-most EST	rlr700899820.h1
Seq. No.	31316
Contig ID	239073_1.R1040
5'-most EST	rlr700899832.h1
Method	BLASTX
NCBI GI	g4006829
BLAST score	188
E value	2.0e-14
Match length	74
% identity	54
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]
Seq. No.	31317
Contig ID	239116_1.R1040
5'-most EST	rlr700899964.h1
Method	BLASTX
NCBI GI	g3355473
BLAST score	152
E value	2.0e-13
Match length	89
% identity	56
NCBI Description	(AC004218) hypothetical protein [Arabidopsis thaliana]
Seq. No.	31318
Contig ID	239175_1.R1040
5'-most EST	zsg701121593.h1
Seq. No.	31319
Contig ID	239185_1.R1040
5'-most EST	rlr700900113.h1
Method	BLASTX
NCBI GI	g3426039
BLAST score	288
E value	4.0e-26
Match length	82
% identity	68
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.	31320
Contig ID	239247_1.R1040
5'-most EST	rlr700900254.h1

Seq. No. 31321
 Contig ID 239299_1.R1040
 5'-most EST g4297487

Seq. No. 31322
 Contig ID 239371_1.R1040
 5'-most EST rlr700900511.h1
 Method BLASTX
 NCBI GI g3355467
 BLAST score 203
 E value 7.0e-16
 Match length 99
 % identity 45
 NCBI Description (AC004218) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31323
 Contig ID 239388_1.R1040
 5'-most EST rlr700900537.h1
 Method BLASTX
 NCBI GI g3096947
 BLAST score 481
 E value 1.0e-48
 Match length 105
 % identity 86
 NCBI Description (Y16327) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]

Seq. No. 31324
 Contig ID 239402_1.R1040
 5'-most EST rlr700900553.h1

Seq. No. 31325
 Contig ID 239407_1.R1040
 5'-most EST rlr700900558.h1
 Method BLASTX
 NCBI GI g2129635
 BLAST score 443
 E value 5.0e-44
 Match length 141
 % identity 62
 NCBI Description light repressible receptor protein kinase - Arabidopsis thaliana >gi_1321686_emb_CAA66376_(X97774) light repressible receptor protein kinase [Arabidopsis thaliana]

Seq. No. 31326
 Contig ID 239451_1.R1040
 5'-most EST rlr700900625.h1
 Method BLASTX
 NCBI GI g1710628
 BLAST score 185
 E value 1.0e-13
 Match length 78
 % identity 15
 NCBI Description HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F) >gi_631210_pir_S43484 hnRNP F protein - human >gi_452048 (L28010) HnRNP F protein [Homo sapiens]

0 1 2 3 4 5 6 7 8 9

Seq. No.	31341
Contig ID	239912_1.R1040
5'-most EST	dpv701101235.h1

```
Seq. No.          31343
Contig ID         239956_1.R1040
5'-most EST      jC-gmro02910027c06a1
Method            BLASTX
NCBI GI           g3335359
BLAST score       188
E value           4.0e-14
Match length      96
% identity        35
NCBI Description  (AC003028) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.          31345
Contig ID         240065_1.R1040
5'-most EST      g4305686
Method            BLASTX
NCBI GI           g2911077
BLAST score       284
E value           2.0e-25
Match length      106
% identity        48
NCBI Description  (AL021960) gibberellin 20-oxidase - like protein
                  [Arabidopsis thaliana]
```

4793

[illegible]

Seq. No. 31365

Seq. No. 31372
 Contig ID 241096_1.R1040
 5'-most EST uC-gmflminsoy045a06b1
 Method BLASTX
 NCBI GI g2129550
 BLAST score 146
 E value 2.0e-09
 Match length 33
 % identity 82
 NCBI Description calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -
 Arabidopsis thaliana >gi_2129554_pir_S71901
 calcium-dependent protein kinase 6 - Arabidopsis thaliana
 >gi_836940 (U20623) calcium-dependent protein kinase
 [Arabidopsis thaliana] >gi_836944 (U20625)
 calcium-dependent protein kinase [Arabidopsis thaliana]
 >gi_4454034_emb_CAA23031.1 (AL035394) calcium-dependent
 protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No. 31373
 Contig ID 241097_1.R1040
 5'-most EST uC-gmrominsoy062e01b1
 Method BLASTX
 NCBI GI g1666096
 BLAST score 249
 E value 3.0e-21
 Match length 89
 % identity 56
 NCBI Description (Y09113) dioxygenase [Marah macrocarpus]

Seq. No. 31374
 Contig ID 241150_1.R1040
 5'-most EST dpv701098766.h2

Seq. No. 31375
 Contig ID 241169_1.R1040
 5'-most EST dpv701097591.h1

Seq. No. 31376
 Contig ID 241230_1.R1040
 5'-most EST uC-gmrominsoy247a11b1
 Method BLASTX
 NCBI GI g2191151
 BLAST score 246
 E value 1.0e-20
 Match length 164
 % identity 35
 NCBI Description (AF007269) contains similarity to membrane associated
 salt-inducible protein [Arabidopsis thaliana]

Seq. No. 31377
 Contig ID 241242_1.R1040
 5'-most EST dpv701097695.h1

Seq. No. 31378
 Contig ID 241259_1.R1040
 5'-most EST g4297977

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NCBI GI	g1575556
BLAST score	224
E value	2.0e-54
Match length	131
% identity	85
NCBI Description	(U66299) acyl-CoA oxidase homolog [Phalaenopsis sp. 'True Lady']
Seq. No.	31399
Contig ID	241794_1.R1040
5'-most EST	uC-gmrominsoy045h04b1
Seq. No.	31400
Contig ID	241850_1.R1040
5'-most EST	dpv701098934.h1
Method	BLASTX
NCBI GI	g2262116
BLAST score	143
E value	6.0e-09
Match length	116
% identity	36
NCBI Description	(AC002343) cellulose synthase isolog [Arabidopsis thaliana]
Seq. No.	31401
Contig ID	241891_1.R1040
5'-most EST	dpv701099004.h1
Seq. No.	31402
Contig ID	241898_1.R1040
5'-most EST	gsv701051813.h1
Seq. No.	31403
Contig ID	241909_1.R1040
5'-most EST	dpv701099026.h1
Seq. No.	31404
Contig ID	241912_1.R1040
5'-most EST	jC-gmst02400062b05d1
Method	BLASTX
NCBI GI	g1346261
BLAST score	240
E value	4.0e-20
Match length	63
% identity	68
NCBI Description	GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR) >gi_1015319_dbj_BAA11091_ (D67088) glutamyl-tRNA reductase [Cucumis sativus]
Seq. No.	31405
Contig ID	241950_1.R1040
5'-most EST	dpv701099090.h1
Seq. No.	31406
Contig ID	241992_1.R1040
5'-most EST	asn701141457.h1
Seq. No.	31407

[illegible]

```
Seq. No.          31409
Contig ID         242047_2.R1040
5'-most EST      uC-gmrnoir024d04b1
Method            BLASTX
NCBI GI           g2388566
BLAST score       222
E value           4.0e-18
Match length      93
% identity        46
NCBI Description  (AC000098) Similar to Arabidopsis Fe(II) transport protein
                  (qb U27590). [Arabidopsis thaliana]
```

```
Seq. No.          31410
Contig ID         242075_1.R1040
5'-most EST      g4290344
Method           BLASTX
NCBI GI          g1781326
BLAST score      372
E value          2.0e-35
Match length     139
% identity       55
NCBI Description  (Y10464) peroxidase [Spinacia oleracea]
```

```
Seq. No.          31411
Contig ID         242091_1.R1040
5'-most EST      dpv701099303.h1
Method            BLASTN
NCBI GI           g166929
BLAST score       70
E value           3.0e-31
Match length      156
% identity        91
NCBI Description  A.thaliana ubiquitin extension protein (UBQ1) gene,
                  complete cds
```

```
Seq. No.          31412
Contig ID         242156_1.R1040
5'-most EST      dpv701099383.h1
Method            BLASTX
NCBI GI           g2642445
BLAST score       205
E value           8.0e-16
Match length      122
```


% identity 43
 NCBI Description (AC002391) putative serine/threonine protein kinase
 [Arabidopsis thaliana]

Seq. No. 31413
 Contig ID 242217_1.R1040
 5'-most EST fua701043047.h1
 Method BLASTX
 NCBI GI g1781279
 BLAST score 151
 E value 4.0e-10
 Match length 62
 % identity 45
 NCBI Description (Y10455) MtN13 [Medicago truncatula]

Seq. No. 31414
 Contig ID 242300_1.R1040
 5'-most EST dpv701099685.h1

Seq. No. 31415
 Contig ID 242328_1.R1040
 5'-most EST dpv701099656.h1

Seq. No. 31416
 Contig ID 242354_1.R1040
 5'-most EST dpv701099701.h1

Seq. No. 31417
 Contig ID 242369_1.R1040
 5'-most EST fua701036913.h1
 Method BLASTN
 NCBI GI g18590
 BLAST score 433
 E value 0.0e+00
 Match length 507
 % identity 100
 NCBI Description G.max GH3 gene for auxin-regulated protein

Seq. No. 31418
 Contig ID 242378_1.R1040
 5'-most EST uC-gmrominsoyl26e03b1

Seq. No. 31419
 Contig ID 242378_2.R1040
 5'-most EST dpv701099729.h1

Seq. No. 31420
 Contig ID 242480_1.R1040
 5'-most EST jC-gmst02400049a09a1
 Method BLASTX
 NCBI GI g2292907
 BLAST score 527
 E value 8.0e-54
 Match length 151
 % identity 34
 NCBI Description (Y10099) P-glycoprotein homologue [Hordeum vulgare]

Seq. No. 31421
 Contig ID 242546_1.R1040
 5'-most EST uC-gmrominsoy256g01b1
 Method BLASTX
 NCBI GI g2920839
 BLAST score 341
 E value 6.0e-32
 Match length 142
 % identity 44
 NCBI Description (U95136) Os-FIERG2 gene product [Oryza sativa]

Seq. No. 31422
 Contig ID 242555_1.R1040
 5'-most EST dpv701099968.h1

Seq. No. 31423
 Contig ID 242592_1.R1040
 5'-most EST uC-gmrominsoy109b10b1
 Method BLASTN
 NCBI GI g3821780
 BLAST score 36
 E value 1.0e-10
 Match length 48
 % identity 65
 NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 31424
 Contig ID 242603_1.R1040
 5'-most EST dpv701100033.h2

Seq. No. 31425
 Contig ID 242608_1.R1040
 5'-most EST dpv701100043.h2

Seq. No. 31426
 Contig ID 242634_1.R1040
 5'-most EST g5508996
 Method BLASTX
 NCBI GI g2088647
 BLAST score 473
 E value 3.0e-47
 Match length 163
 % identity 64
 NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]
 >gi_3158394 (AF036340) LRR-containing F-box protein
 [Arabidopsis thaliana]

Seq. No. 31427
 Contig ID 242758_1.R1040
 5'-most EST dpv701100380.h1
 Method BLASTX
 NCBI GI g3868940
 BLAST score 145
 E value 1.0e-10
 Match length 63
 % identity 57
 NCBI Description (AB015054) Alg2 [Rhizomucor pusillus]

5'-most EST dpv701100579.h1
 Method BLASTX
 NCBI GI g1169892
 BLAST score 177
 E value 3.0e-13
 Match length 65
 % identity 54
 NCBI Description PUTATIVE GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE
 (ISOMERIZING) (HEXOSEPHOSPHATE AMINOTRANSFERASE)
 (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT)
 >gi_1006748_emb_CAA90824_ (Z54140)
 glucosamine-fructose-6-phosphate aminotransferase
 [Schizosaccharomyces pombe] >gi_3560205_emb_CAA20758_
 (AL031536) glucosamine--fructose-6-phosphate
 aminotransferase (isomerizing) [Schizosaccharomyces pombe]

Seq. No. 31441
 Contig ID 243021_1.R1040
 5'-most EST dpv701100648.h1

Seq. No. 31442
 Contig ID 243022_1.R1040
 5'-most EST jC-gmro02800034f04a1
 Method BLASTX
 NCBI GI g2346974
 BLAST score 177
 E value 7.0e-13
 Match length 69
 % identity 58
 NCBI Description (AB006599) ZPT2-12 [Petunia x hybrida]

Seq. No. 31443
 Contig ID 243023_1.R1040
 5'-most EST jC-gmro02910031d02a1
 Method BLASTX
 NCBI GI g1732513
 BLAST score 431
 E value 1.0e-51
 Match length 125
 % identity 79
 NCBI Description (U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]

Seq. No. 31444
 Contig ID 243044_1.R1040
 5'-most EST hrw701062605.h1
 Method BLASTX
 NCBI GI g2342682
 BLAST score 296
 E value 8.0e-27
 Match length 77
 % identity 77
 NCBI Description (AC000106) Contains similarity to Rattus AMP-activated
 protein kinase (gb_X95577). [Arabidopsis thaliana]

Seq. No. 31445
 Contig ID 243049_1.R1040

000101-91048950

5'-most EST dpv701100682.h1

Seq. No. 31446
Contig ID 243054_1.R1040
5'-most EST dpv701100688.h1

Seq. No. 31447
Contig ID 243138_1.R1040
5'-most EST uC-gmronoir029b10b1
Method BLASTX
NCBI GI g3135253
BLAST score 363
E value 2.0e-34
Match length 151
% identity 51
NCBI Description (AC003058) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 31448
Contig ID 243184_1.R1040
5'-most EST fC-gmse7000756053r1
Method BLASTX
NCBI GI g4006914
BLAST score 206
E value 4.0e-16
Match length 56
% identity 73
NCBI Description (Z99708) serine C-palmitoyltransferase like protein [Arabidopsis thaliana]

Seq. No. 31449
Contig ID 243237_1.R1040
5'-most EST jC-gmle01810018a01a2
Method BLASTX
NCBI GI g4455334
BLAST score 189
E value 3.0e-14
Match length 119
% identity 37
NCBI Description (AL035525) myosin-like protein [Arabidopsis thaliana]

Seq. No. 31450
Contig ID 243261_1.R1040
5'-most EST dpv701100953.h1

Seq. No. 31451
Contig ID 243330_1.R1040
5'-most EST jC-gmro02800034h07a1

Seq. No. 31452
Contig ID 243360_1.R1040
5'-most EST jC-gmro02800040f02a1

Seq. No. 31453
Contig ID 243368_1.R1040
5'-most EST jC-gmro02910008g11a1

09584016 101000

Seq. No. 31454
 Contig ID 243373_1.R1040
 5'-most EST uC-gmrominsoy087a03b1
 Method BLASTN
 NCBI GI g169980
 BLAST score 438
 E value 0.0e+00
 Match length 446
 % identity 100
 NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No. 31455
 Contig ID 243460_1.R1040
 5'-most EST zsg701127693.h1

Seq. No. 31456
 Contig ID 243463_1.R1040
 5'-most EST uC-gmropic105h10b1
 Method BLASTX
 NCBI GI g4263784
 BLAST score 265
 E value 3.0e-23
 Match length 67
 % identity 70
 NCBI Description (AC006068) putative glycogenin-2 protein [Arabidopsis thaliana]

Seq. No. 31457
 Contig ID 243464_1.R1040
 5'-most EST uC-gmrominsoy182b03b1

Seq. No. 31458
 Contig ID 243542_1.R1040
 5'-most EST dpv701101402.h1
 Method BLASTX
 NCBI GI g4469009
 BLAST score 181
 E value 2.0e-13
 Match length 81
 % identity 49
 NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 31459
 Contig ID 243599_1.R1040
 5'-most EST dpv701103581.h1
 Method BLASTX
 NCBI GI g2879799
 BLAST score 138
 E value 1.0e-08
 Match length 34
 % identity 79
 NCBI Description (AL021813) 60s ribosomal protein [Schizosaccharomyces pombe]

Seq. No. 31460
 Contig ID 243662_1.R1040
 5'-most EST uC-gmrominsoy110h12b1

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

E value 9.0e-34
 Match length 113
 % identity 59
 NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31497
 Contig ID 245173_1.R1040
 5'-most EST uC-gmrominsoy248f11b1

Seq. No. 31498
 Contig ID 245240_1.R1040
 5'-most EST fua701037513.h1

Seq. No. 31499
 Contig ID 245253_1.R1040
 5'-most EST xzy700966706.h1

Seq. No. 31500
 Contig ID 245347_1.R1040
 5'-most EST xzy700966827.h1
 Method BLASTX
 NCBI GI g3116212
 BLAST score 365
 E value 5.0e-35
 Match length 79
 % identity 89
 NCBI Description (AB004797) homeobox gene [Nicotiana tabacum]

Seq. No. 31501
 Contig ID 245395_1.R1040
 5'-most EST xzy700966883.h1

Seq. No. 31502
 Contig ID 245399_1.R1040
 5'-most EST jC-gmro02910037g11a1

Seq. No. 31503
 Contig ID 245413_1.R1040
 5'-most EST fua701036906.h1

Seq. No. 31504
 Contig ID 245429_1.R1040
 5'-most EST fua701036924.h1
 Method BLASTX
 NCBI GI g1946355
 BLAST score 299
 E value 2.0e-27
 Match length 93
 % identity 65
 NCBI Description (U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No. 31505
 Contig ID 245434_1.R1040
 5'-most EST jsh701063843.h1

Seq. No. 31514
 Contig ID 245609_1.R1040
 5'-most EST jC-gmro02910022e08a1
 Method BLASTX
 NCBI GI g3269301
 BLAST score 288
 E value 3.0e-47
 Match length 148
 % identity 63
 NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 31515
 Contig ID 245614_1.R1040
 5'-most EST uC-gmro0minsoy194d08b1
 Method BLASTX
 NCBI GI g3860266
 BLAST score 147
 E value 2.0e-09
 Match length 85
 % identity 18
 NCBI Description (AC005824) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31516
 Contig ID 245623_1.R1040
 5'-most EST fua701037159.h1
 Method BLASTX
 NCBI GI g3941524
 BLAST score 400
 E value 3.0e-39
 Match length 83
 % identity 83
 NCBI Description (AF062916) putative transcription factor [Arabidopsis thaliana]

Seq. No. 31517
 Contig ID 245645_1.R1040
 5'-most EST fua701037181.h1
 Method BLASTX
 NCBI GI g3395440
 BLAST score 295
 E value 9.0e-27
 Match length 95
 % identity 57
 NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31518
 Contig ID 245688_1.R1040
 5'-most EST jC-gmst02400027f08d1
 Method BLASTX
 NCBI GI g2606077
 BLAST score 261
 E value 1.0e-22
 Match length 74
 % identity 62
 NCBI Description (AF030301) auxin-induced protein [Helianthus annuus]

0968-4075

Seq. No.	31539
Contig ID	246404_1.R1040
5'-most EST	asn701138624.h1

```
Seq. No.          31541
Contig ID         246436_1.R1040
5'-most EST -----|C-gmf102220093a06a1
```

Seq. No.	31542
Contig ID	246438_1.R1040
5'-most EST	fua701038275.h1

```
Seq. No.          31544
Contig ID         246509_1.R1040
5'-most EST      jC-gmst02400041e03a1
Method            BLASTX
NCBI GI           g2213602
BLAST score       152
E value           7.0e-10
Match length      52
% identity        62
NCBI Description  (AC000348) T7N9.22 [Arabidopsis thaliana]
```

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Seq. No.	31546
Contig ID	246575_1.R1040
5'-most EST	jC-gmlē01810060e09d1

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Seq. No.          31547
Contig ID         246589_1.R1040
5'-most EST      fua701038535.h1
Method           BLASTX
NCBI GI          g3892050
BLAST score      200
E value          2.0e-15
Match length     96
% identity       54
NCBI Description  (AC002330) hypothetical protein [Arabidopsis thaliana]
```

Seq. No.	31548
Contig ID	246621_1.R1040
5'-most EST	uC-gmrominsoy133h11b1
Method	BLASTX
NCBI GI	g3786007
BLAST score	159
E value	1.0e-10
Match length	114
% identity	33
NCBI Description	(AC005499) hypothetical protein [Arabidopsis thaliana]

```
Seq. No.          31549
Contig ID         246642_1.R1040
5'-most EST      uC-gmfl̄minsoy044d11b1
Method            BLASTX
NCBI GI           g3953470
BLAST score       146
E value           5.0e-09
Match length      89
% identity        40
NCBI Description  (AC002328) F20N2.15 [Arabidopsis thaliana]
```

Seq. No.	31550
Contig ID	246704_1.R1040
5'-most EST	uC-gmrominsoy236e08b1

```
Seq. No.          31551
Contig ID         246800_1.R1040
5'-most EST      jC-gmr02910061b06a1
Method            BLASTX
NCBI GI           g1403134
BLAST score       278
E value           1.0e-24
Match length      117
```


% identity 53
 NCBI Description (X98453) peroxidase [Arabidopsis thaliana]

Seq. No. 31552
 Contig ID 246807_1.R1040
 5'-most EST fua701038813.h1

Seq. No. 31553
 Contig ID 246840_1.R1040
 5'-most EST uC-gmronoir0001g01b1
 Method BLASTX
 NCBI GI g2262178
 BLAST score 388
 E value 3.0e-37
 Match length 141
 % identity 58
 NCBI Description (AC002329) putative Mlo-like protein [Arabidopsis thaliana]

Seq. No. 31554
 Contig ID 246841_1.R1040
 5'-most EST jC-gmst02400060c06a1

Seq. No. 31555
 Contig ID 246860_1.R1040
 5'-most EST kll701211237.h1

Seq. No. 31556
 Contig ID 246957_1.R1040
 5'-most EST fua701039013.h1

Seq. No. 31557
 Contig ID 246971_1.R1040
 5'-most EST fua701039063.h1

Seq. No. 31558
 Contig ID 247066_1.R1040
 5'-most EST g5753703
 Method BLASTX
 NCBI GI g3695019
 BLAST score 599
 E value 3.0e-62
 Match length 173
 % identity 65
 NCBI Description (AF055848) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 31559
 Contig ID 247068_1.R1040
 5'-most EST uC-gmfllminsoy053d03b1
 Method BLASTX
 NCBI GI g2052510
 BLAST score 603
 E value 9.0e-63
 Match length 138
 % identity 80
 NCBI Description (U95758) lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Arabidopsis thaliana]

NCBI Description (X94443) pectinmethylesterase [*Vigna radiata*]

Seq. No. 31569
Contig ID 247490_1.R1040
5'-most EST gsv701046837.h1

Seq. No. 31570
Contig ID 247523_1.R1040
5'-most EST fua701039911.h1

Seq. No. 31571
Contig ID 247533_1.R1040
5'-most EST fua701039923.h1
Method BLASTX
NCBI GI g4151319
BLAST score 240
E value 2.0e-20
Match length 52
% identity 90

NCBI Description (AF089084) putative auxin efflux carrier protein; AtPIN1
[*Arabidopsis thaliana*]

Seq. No. 31572
Contig ID 247548_1.R1040
5'-most EST jC-gmfl02220080a04d1

Seq. No. 31573
Contig ID 247553_1.R1040
5'-most EST fua701039971.h1
Method BLASTX
NCBI GI g2829910
BLAST score 147
E value 1.0e-09
Match length 84
% identity 45

NCBI Description (AC002291) Unknown protein, contains regulator of
chromosome condensation motifs [*Arabidopsis thaliana*]

Seq. No. 31574
Contig ID 247667_1.R1040
5'-most EST fua701040157.h1

Seq. No. 31575
Contig ID 247674_1.R1040
5'-most EST fua701040166.h1
Method BLASTX
NCBI GI g1002800
BLAST score 629
E value 2.0e-65
Match length 139
% identity 82

NCBI Description (U33917) Cpm7 [*Craterostigma plantagineum*]

Seq. No. 31576
Contig ID 247708_1.R1040
5'-most EST epx701108580.h1
Method BLASTX

Seq. No. 31615
 Contig ID 248756_1.R1040
 5'-most EST jC-gmst02400050h11a1

Seq. No. 31616
 Contig ID 248764_1.R1040
 5'-most EST fua701041707.h1

Seq. No. 31617
 Contig ID 248771_1.R1040
 5'-most EST fua701041815.h1
 Method BLASTX
 NCBI GI g2924509
 BLAST score 403
 E value 1.0e-39
 Match length 88
 % identity 86
 NCBI Description (AL022023) subtilisin proteinase - like [Arabidopsis thaliana]

Seq. No. 31618
 Contig ID 248780_1.R1040
 5'-most EST fua701041824.h1

Seq. No. 31619
 Contig ID 248805_1.R1040
 5'-most EST fua701041754.h1

Seq. No. 31620
 Contig ID 248807_1.R1040
 5'-most EST fua701041856.h1
 Method BLASTX
 NCBI GI g100226
 BLAST score 174
 E value 8.0e-13
 Match length 92
 % identity 42
 NCBI Description hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf_1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No. 31621
 Contig ID 248818_1.R1040
 5'-most EST fua701041767.h1
 Method BLASTX
 NCBI GI g116337
 BLAST score 262
 E value 4.0e-23
 Match length 83
 % identity 60
 NCBI Description BASIC ENDOCHITINASE PRECURSOR >gi_100310_pir_S23545 chitinase (EC 3.2.1.14) III, basic - common tobacco >gi_19803_emb_CAA77657_ (Z11564) basic chitinase III [Nicotiana tabacum]

Seq. No. 31622

NFX1 - human >gi_563217 (U15306) NFX1 [Homo sapiens]
 >gi_4505387_ref_NP_002495.1_pNFX1_nuclear transcription
 factor, X-box binding

Seq. No. 31629
 Contig ID 249006_1.R1040
 5'-most EST uC-gmrominsoy192a04b1
 Method BLASTX
 NCBI GI g2335096
 BLAST score 355
 E value 1.0e-33
 Match length 156
 % identity 48
 NCBI Description (AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 31630
 Contig ID 249016_1.R1040
 5'-most EST jC-gmro02910051e06a1
 Method BLASTX
 NCBI GI g119351
 BLAST score 209
 E value 1.0e-16
 Match length 51
 % identity 82
 NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
 (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_84950_pir_S07586
 phosphopyruvate hydratase (EC 4.2.1.11) - fruit fly
 (Drosophila melanogaster) >gi_7946_emb_CAA34895_ (X17034)
 enolase (AA 1-433) [Drosophila melanogaster]

Seq. No. 31631
 Contig ID 249023_1.R1040
 5'-most EST leu701144413.h1

Seq. No. 31632
 Contig ID 249058_2.R1040
 5'-most EST fua701042108.h1
 Method BLASTX
 NCBI GI g3695392
 BLAST score 160
 E value 1.0e-10
 Match length 35
 % identity 80
 NCBI Description (AF096371) No definition line found [Arabidopsis thaliana]

Seq. No. 31633
 Contig ID 249119_1.R1040
 5'-most EST uC-gmrominsoy044h11b1
 Method BLASTX
 NCBI GI g3176686
 BLAST score 706
 E value 1.0e-74
 Match length 169
 % identity 75
 NCBI Description (AC003671) Similar to high affinity potassium transporter,
 HAK1 protein gb_U22945 from Schwanniomyces occidentalis.
 [Arabidopsis thaliana]

Seq. No. 31634
 Contig ID 249129_1.R1040
 5'-most EST jsh701067681.h1
 Method BLASTX
 NCBI GI g4008372
 BLAST score 193
 E value 7.0e-15
 Match length 113
 % identity 37
 NCBI Description (Z27079) cDNA EST CEMSF67FB comes from this gene; cDNA EST CEMSF67R comes from this gene; cDNA EST yk195e10.3 comes from this gene; cDNA EST yk195e10.5 comes from this gene; cDNA EST yk397a5.3 comes from this gene; cDNA EST yk3

Seq. No. 31635
 Contig ID 249180_1.R1040
 5'-most EST g4397143
 Method BLASTN
 NCBI GI g169348
 BLAST score 144
 E value 5.0e-75
 Match length 276
 % identity 22
 NCBI Description P.vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end

Seq. No. 31636
 Contig ID 249237_1.R1040
 5'-most EST jC-gmro02910073h08a1
 Method BLASTX
 NCBI GI g4063742
 BLAST score 320
 E value 2.0e-29
 Match length 176
 % identity 48
 NCBI Description (AC005851) putative phaseolin G-box binding protein [Arabidopsis thaliana]

Seq. No. 31637
 Contig ID 249241_1.R1040
 5'-most EST uC-gmropic075e12b1

Seq. No. 31638
 Contig ID 249241_2.R1040
 5'-most EST gsv701049418.h1

Seq. No. 31639
 Contig ID 249275_1.R1040
 5'-most EST fua701042384.h1

Seq. No. 31640
 Contig ID 249313_1.R1040
 5'-most EST fua701042540.h1

Seq. No. 31641
 Contig ID 249323_1.R1040

069-071-101000

Seq. No.	31643
Contig ID	249369_1.R1040
5'-most EST	fua701042610.h1

```
Seq. No.          31644
Contig ID         249386_1.R1040
5'-most EST      fua701042629.h1
Method            BLASTX
NCBI GI           g3924604
BLAST score       346
E value           1.0e-32
Match length      89
% identity        74
NCBI Description  (AF069442) putative leucine-rich repeat protein
                  [Arabidopsis thaliana]
```

```
Seq. No.          31646
Contig ID         249515_1.R1040
5'-most EST      fua701043364.h1
Method            BLASTX
NCBI GI           g129813
BLAST score       192
E value           6.0e-15
Match length      77
% identity         49
NCBI Description  PEROXIDASE C1A PRECURSOR >gi_2144377_pir__OPRHC peroxidase
                  (EC 1.11.1.7) C1 precursor - horseradish
```

Seq. No.	31647
Contig ID	249570_1.R1040
5'-most EST	leu701151908.h1

Seq. No.	31648
Contig ID	249592_1.R1040
5'-most EST	jC-qmro02910024h02d1

```
Seq. No.          31649
Contig ID         249609_1.R1040
5'-most EST      uC-gmfIminsoy061h06b1
Method           BLASTX
NCBI GI          g2497539
BLAST score       322
E value          4.0e-30
Match length      76
% identity        79
NCBI Description  PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi_169703
                  (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]
```


Seq. No. 31650
 Contig ID 249705_1.R1040
 5'-most EST jC-gmro02910051a02a1
 Method BLASTX
 NCBI GI g2492820
 BLAST score 253
 E value 2.0e-21
 Match length 104
 % identity 41
 NCBI Description HYPOTHETICAL 54.0 KD PROTEIN IN NRGA-USD INTERGENIC REGION
 >gi_1684649_emb_CAB05378_(Z82987) unknown, similar to
 uracil permease from Schizosaccharomyces pombe [Bacillus
 subtilis] >gi_2636172_emb_CAB15664.1_(Z99122) similar to
 permease [Bacillus subtilis]

Seq. No. 31651
 Contig ID 249731_1.R1040
 5'-most EST leu701150624.h1

Seq. No. 31652
 Contig ID 249784_1.R1040
 5'-most EST asn701142062.h1

Seq. No. 31653
 Contig ID 249811_1.R1040
 5'-most EST fua701043283.h1

Seq. No. 31654
 Contig ID 249817_1.R1040
 5'-most EST fua701043290.h1
 Method BLASTX
 NCBI GI g3540183
 BLAST score 407
 E value 8.0e-40
 Match length 138
 % identity 59
 NCBI Description (AC004122) Highly Similar to branched-chain amino acid
 aminotransferase [Arabidopsis thaliana]

Seq. No. 31655
 Contig ID 249827_1.R1040
 5'-most EST fua701043305.h1
 Method BLASTN
 NCBI GI g3860320
 BLAST score 92
 E value 2.0e-44
 Match length 258
 % identity 85
 NCBI Description Cicer arietinum mRNA for beta-galactosidase, clone
 CanBGal-5

Seq. No. 31656
 Contig ID 249832_1.R1040
 5'-most EST leu701145936.h1
 Method BLASTN
 NCBI GI g2598574

09684015-101000

BLAST score 114
E value 4.0e-57
Match length 358
% identity 83
NCBI Description Medicago truncatula mRNA for MtN21 gene

Seq. No. 31657
Contig ID 249838_1.R1040
5'-most EST jC-gmf102220053e06a1
Method BLASTX
NCBI GI g3152566
BLAST score 309
E value 3.0e-28
Match length 148
% identity 45
NCBI Description (AC002986) Similar to hypothetical protein YLR002c, gb_Z7314 from S. cerevisiae. [Arabidopsis thaliana]

Seq. No. 31658
Contig ID 249860_1.R1040
5'-most EST k11701211805.h1

Seq. No. 31659
Contig ID 249915_1.R1040
5'-most EST fua701043414.h1
Method BLASTX
NCBI GI g1791307
BLAST score 570
E value 1.0e-58
Match length 198
% identity 57
NCBI Description (U83501) permease homolog [Arabidopsis thaliana]

Seq. No. 31660
Contig ID 249980_1.R1040
5'-most EST lus701015749.h1

Seq. No. 31661
Contig ID 249990_1.R1040
5'-most EST asn701131156.h1

Seq. No. 31662
Contig ID 250041_1.R1040
5'-most EST fC-gmro700564066f2

Seq. No. 31663
Contig ID 250063_1.R1040
5'-most EST fua701043589.h1

Seq. No. 31664
Contig ID 250069_1.R1040
5'-most EST hrw701060533.h1

Seq. No. 31665
Contig ID 250074_1.R1040
5'-most EST k11701202347.h1
Method BLASTX

NCBI GI g557472
 BLAST score 234
 E value 2.0e-19
 Match length 148
 % identity 39
 NCBI Description (U15178) arabinosidase [Bacteroides ovatus]

Seq. No. 31666
 Contig ID 250082_1.R1040
 5'-most EST jC-gmst02400071f09a1
 Method BLASTX
 NCBI GI g3281861
 BLAST score 557
 E value 3.0e-57
 Match length 177
 % identity 62
 NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 31667
 Contig ID 250112_1.R1040
 5'-most EST fua701043660.h1
 Method BLASTX
 NCBI GI g3859112
 BLAST score 231
 E value 3.0e-19
 Match length 56
 % identity 75
 NCBI Description (AF031607) male sterility MS5 [Arabidopsis thaliana]

Seq. No. 31668
 Contig ID 250116_1.R1040
 5'-most EST jC-gmle01810021d02a1

Seq. No. 31669
 Contig ID 250117_1.R1040
 5'-most EST fua701043666.h1

Seq. No. 31670
 Contig ID 250129_1.R1040
 5'-most EST uC-gmf1minsoy031d08b1
 Method BLASTX
 NCBI GI g3329368
 BLAST score 430
 E value 2.0e-42
 Match length 175
 % identity 53
 NCBI Description (AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 31671
 Contig ID 250134_1.R1040
 5'-most EST fua701043686.h1

Seq. No. 31672
 Contig ID 250144_1.R1040
 5'-most EST yzl700966904.h1
 Method BLASTX
 NCBI GI g2765821

0960168

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Seq. No.          31680
Contig ID         250355_1.R1040
5'-most EST      leu701152742.h1
Method            BLASTX
NCBI GI           g3047114
BLAST score       149
E value           8.0e-10
Match length      44
% identity        66
NCBI Description  (AF058919) No definition line found [Arabidopsis thaliana]
```

Seq. No.	31682
Contig ID	250388_1.R1040
5'-most EST	asj700967463.h1

Seq. No.	31683
Contig ID	250428_1.R1040
5'-most EST	leu701144353.h1

```
Seq. No.          31684
Contig ID         250485_1.R1040
5'-most EST      leu701156763.h1
Method            BLASTX
NCBI GI           g3757525
BLAST score       413
E value           3.0e-40
Match length      184
% identity        51
NCBI Description  (AC005167) tetracycline transporter-like protein, 3'
                  partial [Arabidopsis thaliana]
```

Seq. No.	31685
Contig ID	250497_1.R1040
5'-most EST	leu701156076.h1

4840

NCBI GI g4454484
 BLAST score 370
 E value 2.0e-35
 Match length 126
 % identity 61
 NCBI Description (AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]

Seq. No. 31687
 Contig ID 250569_1.R1040
 5'-most EST g5058429
 Method BLASTX
 NCBI GI g3540182
 BLAST score 183
 E value 2.0e-13
 Match length 106
 % identity 44
 NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 31688
 Contig ID 250624_1.R1040
 5'-most EST leu701154368.h1

Seq. No. 31689
 Contig ID 250662_1.R1040
 5'-most EST leu701144823.h1

Seq. No. 31690
 Contig ID 250667_1.R1040
 5'-most EST leu701144826.h1

Seq. No. 31691
 Contig ID 250686_1.R1040
 5'-most EST leu701150509.h1
 Method BLASTX
 NCBI GI g3075399
 BLAST score 230
 E value 2.0e-19
 Match length 81
 % identity 56
 NCBI Description (AC004484) SF16-like protein [Arabidopsis thaliana]

Seq. No. 31692
 Contig ID 250760_1.R1040
 5'-most EST leu701145018.h1
 Method BLASTX
 NCBI GI g282964
 BLAST score 308
 E value 2.0e-28
 Match length 67
 % identity 76
 NCBI Description transforming protein (myb) homolog (clone myb.Ph3) - garden petunia >gi_20563_emb_CAA78386_ (Z13996) protein 1 [Petunia x hybrida]

Seq. No. 31693
 Contig ID 250806_1.R1040

09864015 10100

```
Seq. No.          31735
Contig ID         252475_1.R1040
5'-most EST      leu701150839.h1
Method            BLASTX
NCBI GI           g3292829
BLAST score       160
E value           4.0e-11
Match length      75
% identity        48
NCBI Description  (AL031018) putative protein [Arabidopsis thaliana]
```

```
Seq. No.          31737
Contig ID         252606_1.R1040
5'-most EST      leu701147908.h1
Method            BLASTX
NCBI GI           g2244784
BLAST score       388
E value           1.0e-37
Match length      133
% identity        63
NCBI Description  (Z97335) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.          31739
Contig ID         252811_1.R1040
5'-most EST      leu701148184.h1
Method            BLASTX
NCBI GI           g1653395
BLAST score       247
```


% identity 67
 NCBI Description hypothetical protein YPL093w - yeast (*Saccharomyces cerevisiae*) >gi_1151233 (U43281) Lpg15p [*Saccharomyces cerevisiae*]

Seq. No. 31763
 Contig ID 253628_1.R1040
 5'-most EST leu701150093.h1

Seq. No. 31764
 Contig ID 253645_1.R1040
 5'-most EST asn701134216.h1
 Method BLASTX
 NCBI GI g2335100
 BLAST score 474
 E value 8.0e-48
 Match length 112
 % identity 79
 NCBI Description (AC002339) unknown protein [*Arabidopsis thaliana*]

Seq. No. 31765
 Contig ID 253699_1.R1040
 5'-most EST leu701151830.h1

Seq. No. 31766
 Contig ID 253700_1.R1040
 5'-most EST leu701149508.h1
 Method BLASTN
 NCBI GI g3128136
 BLAST score 39
 E value 2.0e-12
 Match length 51
 % identity 94
 NCBI Description *Arabidopsis thaliana* genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [*Arabidopsis thaliana*]

Seq. No. 31767
 Contig ID 253791_1.R1040
 5'-most EST kl1701213583.h1
 Method BLASTX
 NCBI GI g2213629
 BLAST score 258
 E value 1.0e-22
 Match length 52
 % identity 88
 NCBI Description (AC000103) F21J9.21 [*Arabidopsis thaliana*]

Seq. No. 31768
 Contig ID 253867_1.R1040
 5'-most EST leu701149741.h1

Seq. No. 31769
 Contig ID 253887_1.R1040
 5'-most EST leu701149768.h1

Seq. No. 31770
 Contig ID 253934_1.R1040

Seq. No. 31781
 Contig ID 254385_1.R1040
 5'-most EST leu701151904.h1

Seq. No. 31782
 Contig ID 254471_1.R1040
 5'-most EST uC-gmrominsoy034c12b1

Seq. No. 31783
 Contig ID 254488_1.R1040
 5'-most EST gsv701047738.h1

Seq. No. 31784
 Contig ID 254530_1.R1040
 5'-most EST jC-gmf102220051g07a1

Seq. No. 31785
 Contig ID 254541_1.R1040
 5'-most EST leu701150790.h1
 Method BLASTX
 NCBI GI g3402692
 BLAST score 338
 E value 8.0e-32
 Match length 82
 % identity 79
 NCBI Description (AC004697) putative
 CDP-diacylglycerol--glycerol-3-phosphate
 3-phosphatidyltransferase [Arabidopsis thaliana]

Seq. No. 31786
 Contig ID 254630_1.R1040
 5'-most EST leu701155825.h1

Seq. No. 31787
 Contig ID 254654_1.R1040
 5'-most EST g5606123
 Method BLASTX
 NCBI GI g4455202
 BLAST score 671
 E value 6.0e-73
 Match length 210
 % identity 64
 NCBI Description (AL035440) putative APG protein [Arabidopsis thaliana]

Seq. No. 31788
 Contig ID 254798_1.R1040
 5'-most EST leu701151278.h1

Seq. No. 31789
 Contig ID 254815_1.R1040
 5'-most EST asn701139715.h1

Seq. No. 31790
 Contig ID 254959_1.R1040
 5'-most EST gsv701056139.h1

Match length	85
% identity	31
NCBI Description	(AC002339) salt inducible protein-like [Arabidopsis thaliana]
Seq. No.	31799
Contig ID	255151_1.R1040
5'-most EST	leu701151909.h1
Seq. No.	31800
Contig ID	255202_1.R1040
5'-most EST	leu701152071.h1
Seq. No.	31801
Contig ID	255206_1.R1040
5'-most EST	leu701151982.h1
Method	BLASTN
NCBI GI	g3860320
BLAST score	161
E value	1.0e-85
Match length	249
% identity	91
NCBI Description	Cicer arietinum mRNA for beta-galactosidase, clone CanBGal-5
Seq. No.	31802
Contig ID	255219_1.R1040
5'-most EST	leu701152005.h1
Seq. No.	31803
Contig ID	255234_1.R1040
5'-most EST	leu701152032.h1
Seq. No.	31804
Contig ID	255287_1.R1040
5'-most EST	epx701108938.h1
Method	BLASTN
NCBI GI	g3021354
BLAST score	131
E value	1.0e-67
Match length	299
% identity	86
NCBI Description	Cyamopsis tetragonoloba mRNA for UDP-galactose 4-epimerase, clone GEPI42
Seq. No.	31805
Contig ID	255301_1.R1040
5'-most EST	leu701152137.h1
Seq. No.	31806
Contig ID	255307_1.R1040
5'-most EST	leu701152188.h1
Seq. No.	31807
Contig ID	255346_1.R1040
5'-most EST	leu701152226.h1

5'-most EST leu701152950.h1

Seq. No. 31818
 Contig ID 255786_1.R1040
 5'-most EST leu701152986.h1
 Method BLASTX
 NCBI GI g1946366
 BLAST score 410
 E value 2.0e-40
 Match length 106
 % identity 77
 NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 31819
 Contig ID 255791_1.R1040
 5'-most EST leu701152993.h1

Seq. No. 31820
 Contig ID 255798_1.R1040
 5'-most EST leu701153008.h1

Seq. No. 31821
 Contig ID 255861_1.R1040
 5'-most EST gsv701052033.h1

Seq. No. 31822
 Contig ID 255870_1.R1040
 5'-most EST leu701153136.h1

Seq. No. 31823
 Contig ID 255877_1.R1040
 5'-most EST leu701153464.h1

Seq. No. 31824
 Contig ID 255909_1.R1040
 5'-most EST g5126284

Seq. No. 31825
 Contig ID 255958_1.R1040
 5'-most EST g4277036
 Method BLASTX
 NCBI GI g3482919
 BLAST score 246
 E value 6.0e-21
 Match length 77
 % identity 68
 NCBI Description (AC003970) Putative protein kinase [Arabidopsis thaliana]

Seq. No. 31826
 Contig ID 255964_1.R1040
 5'-most EST jC-gmle01810048b11a1

Seq. No. 31827
 Contig ID 255981_1.R1040
 5'-most EST leu701155318.h1

Seq. No. 31828

Contig ID 255989 1.R1040
5'-most EST leu701153444.h1

Seq. No. 31829
Contig ID 255995 1.R1040
5'-most EST leu701157044.h1

Seq. No. 31830
Contig ID 256053 1.R1040
5'-most EST leu701153536.h1
Method BLASTX
NCBI GI g82056
BLAST score 346
E value 4.0e-33
Match length 81
% identity 84
NCBI Description protein kinase, calcium-dependent (EC 2.7.1.-) - carrot (fragment)

Seq. No. 31831
Contig ID 256065 1.R1040
5'-most EST leu701154631.h1

Seq. No. 31832
Contig ID 256067 1.R1040
5'-most EST leu701157703.h1
Method BLASTX
NCBI GI g4455202
BLAST score 198
E value 1.0e-15
Match length 49
% identity 73
NCBI Description (AL035440) putative APG protein [Arabidopsis thaliana]

Seq. No. 31833
Contig ID 256103 1.R1040
5'-most EST jC-gms02400048h05a1
Method BLASTX
NCBI GI g4406778
BLAST score 424
E value 4.0e-42
Match length 90
% identity 87
NCBI Description (AC006532) putative brassinosteroid insensitive protein [Arabidopsis thaliana]

Seq. No. 31834
Contig ID 256105 1.R1040
5'-most EST leu701153775.h1
Method BLASTN
NCBI GI g3599418
BLAST score 33
E value 3.0e-09
Match length 58
% identity 90
NCBI Description Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds

Seq. No. 31840
Contig ID 256562_1.R1040
5'-most EST leu701154463.h1

Seq. No. 31841
Contig ID 256640_1.R1040
5'-most EST leu701154583.h1

Seq. No. 31842
Contig ID 256660_1.R1040
5'-most EST leu701154616.h1

Seq. No. 31843
Contig ID 256677_1.R1040
5'-most EST gsv701051142.h1

Seq. No. 31844
Contig ID 256686_1.R1040
5'-most EST leu701154688.h1
Method BLASTX
NCBI GI g3892052
BLAST score 143
E value 3.0e-09
Match length 72
% identity 43
NCBI Description (AC002330) predicted protein of unknown function
[Arabidopsis thaliana]

Seq. No. 31845
Contig ID 256696_1.R1040
5'-most EST kll701212105.h1

Seq. No. 31846
Contig ID 256717_1.R1040
5'-most EST leu701154812.h1
Method BLASTX
NCBI GI g1076715
BLAST score 159
E value 4.0e-11
Match length 51
% identity 57
NCBI Description abscisic acid-induced protein HVA22 - barley >gi_404589
(L19119) A22 [Hordeum vulgare]

Seq. No. 31847
Contig ID 256718_1.R1040
5'-most EST leu701154813.h1

Seq. No. 31848
Contig ID 256780_1.R1040
5'-most EST leu701157246.h1

Seq. No. 31849
Contig ID 256866_1.R1040
5'-most EST leu701155254.h1

Seq. No. 31850

SECRET

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Seq. No.          31881
Contig ID         257834_1.R1040
5'-most EST      k11701209132.h1
Method            BLASTX
NCBI GI           g2959781
BLAST score       316
E value           4.0e-29
Match length      145
% identity        35
NCBI Description  (AJ223508) Zwille protein [Arabidopsis thaliana]
```

```
Seq. No.          31883
Contig ID         257856_1.R1040
5'-most EST      leu701156706.h1
Method           BLASTX
NCBI GI          g3646324
BLAST score       206
E value          1.0e-16
Match length      78
% identity        56
NCBI Description  (AJ000761) MADS-box protein [Malus domestica]
```

```
Seq. No.          31885
Contig ID         257894_1.R1040
5'-most EST      leu701156756.h1
Method            BLASTX
NCBI GI           g2921336
BLAST score       581
E value           5.0e-60
Match length      119
% identity        87
NCBI Description  (AF034132) MYB-like DNA-binding domain protein [Gossypium
                  hirsutum]
```


Seq. No. 31886
 Contig ID 257926_1.R1040
 5'-most EST leu701157083.h1

Seq. No. 31887
 Contig ID 257973_1.R1040
 5'-most EST leu701156974.h1

Seq. No. 31888
 Contig ID 257976_1.R1040
 5'-most EST leu701156988.h1

Seq. No. 31889
 Contig ID 257986_1.R1040
 5'-most EST leu701156994.h1

Seq. No. 31890
 Contig ID 257992_1.R1040
 5'-most EST leu701157008.h1
 Method BLASTX
 NCBI GI g3776559
 BLAST score 436
 E value 2.0e-43
 Match length 106
 % identity 80
 NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi_3482933
 cdc2 protein kinase homolog from A. thaliana BAC
 gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this
 gene. [Arabidopsis thaliana]

Seq. No. 31891
 Contig ID 258018_1.R1040
 5'-most EST leu701157043.h1

Seq. No. 31892
 Contig ID 258054_1.R1040
 5'-most EST leu701157092.h1
 Method BLASTX
 NCBI GI g2623304
 BLAST score 181
 E value 3.0e-13
 Match length 119
 % identity 32
 NCBI Description (AC002409) similar to Medicago nodulin N21 [Arabidopsis
 thaliana]

Seq. No. 31893
 Contig ID 258080_1.R1040
 5'-most EST leu701157163.h1

Seq. No. 31894
 Contig ID 258095_1.R1040
 5'-most EST leu701157186.h1

Seq. No. 31895
 Contig ID 258096_1.R1040
 5'-most EST leu701157204.h1

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5'-most EST g5175517
 Method BLASTX
 NCBI GI g2529677
 BLAST score 148
 E value 1.0e-09
 Match length 37
 % identity 73
 NCBI Description (AC002535) kinesin-like protein, heavy chain [Arabidopsis thaliana]

Seq. No. 31983
 Contig ID 262777_1.R1040
 5'-most EST jC-gmro02800027d11d1
 Method BLASTX
 NCBI GI g2739378
 BLAST score 141
 E value 8.0e-09
 Match length 63
 % identity 48
 NCBI Description (AC002505) AR781 [Arabidopsis thaliana]

Seq. No. 31984
 Contig ID 262855_1.R1040
 5'-most EST jC-gmro02910007b01a1

Seq. No. 31985
 Contig ID 262865_1.R1040
 5'-most EST gsv701049586.h1

Seq. No. 31986
 Contig ID 262925_1.R1040
 5'-most EST jC-gmfl02220103e08a1

Seq. No. 31987
 Contig ID 262932_1.R1040
 5'-most EST uC-gmrominsoyl78c11b1

Seq. No. 31988
 Contig ID 262946_1.R1040
 5'-most EST gsv701049693.h1
 Method BLASTX
 NCBI GI g1946368
 BLAST score 258
 E value 2.0e-22
 Match length 119
 % identity 48
 NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 31989
 Contig ID 263020_1.R1040
 5'-most EST g5753325
 Method BLASTX
 NCBI GI g3367531
 BLAST score 131
 E value 7.0e-12
 Match length 148
 % identity 36

NCBI Description (AC004392) Strong similarity to gi_2160138 F19K23.6 gene product from A. thaliana BAC gb_AC000375. [Arabidopsis thaliana]

Seq. No. 31990
Contig ID 263102_1.R1040
5'-most EST gsv701049942.h1
Method BLASTN
NCBI GI g169980
BLAST score 188
E value 1.0e-101
Match length 282
% identity 92
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No. 31991
Contig ID 263175_1.R1040
5'-most EST gsv701051306.h1

Seq. No. 31992
Contig ID 263203_1.R1040
5'-most EST gsv701050068.h1
Method BLASTX
NCBI GI g2827621
BLAST score 194
E value 4.0e-15
Match length 38
% identity 82
NCBI Description (AL021636) putative protein. [Arabidopsis thaliana]

Seq. No. 31993
Contig ID 263309_1.R1040
5'-most EST g5753498
Method BLASTX
NCBI GI g2191168
BLAST score 147
E value 7.0e-21
Match length 91
% identity 60
NCBI Description (AF007270) contains similarity to myosin heavy chain [Arabidopsis thaliana]

Seq. No. 31994
Contig ID 263364_1.R1040
5'-most EST zsg701124991.h1

Seq. No. 31995
Contig ID 263422_1.R1040
5'-most EST gsv701050367.h1

Seq. No. 31996
Contig ID 263439_1.R1040
5'-most EST g5058204
Method BLASTX
NCBI GI g4038044
BLAST score 235
E value 2.0e-19

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Contig ID 263747_1.R1040
5'-most EST k11701213958.h1
Method BLASTX
NCBI GI g2335100
BLAST score 470
E value 2.0e-47
Match length 108
% identity 81
NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]

Seq. No. 32007
Contig ID 263777_1.R1040
5'-most EST gsv701050836.h1
Method BLASTX
NCBI GI g3482920
BLAST score 251
E value 2.0e-21
Match length 63
% identity 73
NCBI Description (AC003970) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 32008
Contig ID 263822_1.R1040
5'-most EST jC-gmf102220080c07a1

Seq. No. 32009
Contig ID 263837_1.R1040
5'-most EST gsv701050960.h1
Method BLASTX
NCBI GI g1800223
BLAST score 150
E value 7.0e-10
Match length 57
% identity 53
NCBI Description (U65018) mannosyltransferase [Dictyostelium discoideum]

Seq. No. 32010
Contig ID 263995_1.R1040
5'-most EST gsv701051161.h1
Method BLASTX
NCBI GI g3668171
BLAST score 422
E value 3.0e-41
Match length 190
% identity 44
NCBI Description (AB006052) RNA polymerase I second-largest subunit [Neurospora crassa]

Seq. No. 32011
Contig ID 264077_1.R1040
5'-most EST uC-gmf1minsoy018b08b1
Method BLASTX
NCBI GI g4455171
BLAST score 262
E value 1.0e-42
Match length 185
% identity 51

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NCBI Description (AL035521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32012
Contig ID 264119_1.R1040
5'-most EST gsv701054444.h1

Seq. No. 32013
Contig ID 264223_1.R1040
5'-most EST fC-gmle700554943d3
Method BLASTX
NCBI GI g2982301
BLAST score 165
E value 2.0e-11
Match length 44
% identity 66

NCBI Description (AF051235) YGL010w-like protein [Picea mariana]

Seq. No. 32014
Contig ID 264286_1.R1040
5'-most EST gsv701051519.h1

Seq. No. 32015
Contig ID 264324_1.R1040
5'-most EST gsv701051566.h1

Seq. No. 32016
Contig ID 264429_1.R1040
5'-most EST gsv701051722.h1
Method BLASTX
NCBI GI g2961346
BLAST score 167
E value 5.0e-12
Match length 37
% identity 76

NCBI Description (AL022140) pectinesterase like protein [Arabidopsis thaliana]

Seq. No. 32017
Contig ID 264454_1.R1040
5'-most EST gsv701056174.h1

Seq. No. 32018
Contig ID 264536_1.R1040
5'-most EST gsv701054288.h1

Seq. No. 32019
Contig ID 264565_1.R1040
5'-most EST gsv701054339.h1

Seq. No. 32020
Contig ID 264566_1.R1040
5'-most EST gsv701051941.h1

Seq. No. 32021
Contig ID 264617_1.R1040
5'-most EST zsg701125604.h1
Method BLASTX

NCBI GI	g4220519
BLAST score	161
E value	5.0e-11
Match length	61
% identity	57
NCBI Description	(AL035356) putative protein binding protein [Arabidopsis thaliana]
Seq. No.	32022
Contig ID	264667_1.R1040
5'-most EST	gsv701052072.h1
Seq. No.	32023
Contig ID	264775_1.R1040
5'-most EST	gsv701052304.h1
Seq. No.	32024
Contig ID	264818_1.R1040
5'-most EST	gsv701052381.h1
Method	BLASTX
NCBI GI	g2262115
BLAST score	449
E value	2.0e-44
Match length	261
% identity	36
NCBI Description	(AC002343) cellulose synthase isolog [Arabidopsis thaliana]
Seq. No.	32025
Contig ID	264961_1.R1040
5'-most EST	gsv701052605.h1
Seq. No.	32026
Contig ID	264986_1.R1040
5'-most EST	uC-gmr0noir000g05b1
Seq. No.	32027
Contig ID	264998_1.R1040
5'-most EST	gsv701052745.h1
Seq. No.	32028
Contig ID	265158_1.R1040
5'-most EST	gsv701052877.h1
Seq. No.	32029
Contig ID	265180_1.R1040
5'-most EST	uC-gmr0pic109h08b1
Seq. No.	32030
Contig ID	265232_1.R1040
5'-most EST	jC-gmf102220063c04d1
Method	BLASTX
NCBI GI	g2281085
BLAST score	315
E value	7.0e-29
Match length	70
% identity	74
NCBI Description	(AC002333) CTR1 protein kinase isolog [Arabidopsis

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thaliana]

Seq. No. 32031
 Contig ID 265232_2.R1040
 5'-most EST fC-gmse700658724d3
 Method BLASTX
 NCBI GI g2281085
 BLAST score 203
 E value 7.0e-16
 Match length 42
 % identity 76
 NCBI Description (AC002333) CTRL protein kinase isolog [Arabidopsis thaliana]

Seq. No. 32032
 Contig ID 265252_1.R1040
 5'-most EST gsv701053004.h1
 Method BLASTX
 NCBI GI g1172633
 BLAST score 179
 E value 2.0e-13
 Match length 91
 % identity 53
 NCBI Description PROLIFERA PROTEIN->gi_675491 (L39954) contains MCM2/3/5 family signature; PROSITE; PS00847; disruption leads to early lethal phenotype; similar to MCM2/3/5 family, most similar to YBR1441 [Arabidopsis thaliana]

Seq. No. 32033
 Contig ID 265256_1.R1040
 5'-most EST uC-gmropic102g10b1
 Method BLASTX
 NCBI GI g1083160
 BLAST score 468
 E value 8.0e-47
 Match length 176
 % identity 51
 NCBI Description mannosyl-oligosaccharide 1,2-alpha-mannosidase (EC 3.2.1.113) - rabbit (fragment)

Seq. No. 32034
 Contig ID 265317_1.R1040
 5'-most EST g5677973

Seq. No. 32035
 Contig ID 265389_1.R1040
 5'-most EST uC-gmrominsoy258f09b1
 Method BLASTX
 NCBI GI g3600039
 BLAST score 374
 E value 5.0e-46
 Match length 201
 % identity 53
 NCBI Description (AF080119) similar to Schizosaccharomyces pombe isp4 protein (GB:D14061) [Arabidopsis thaliana]

Seq. No. 32036

BLAST score 38
 E value 6.0e-12
 Match length 90
 % identity 86
 NCBI Description Pisum sativum mRNA for ftsZ gene

Seq. No. 32056
 Contig ID 266143_1.R1040
 5'-most EST gsv701054229.h1

Seq. No. 32057
 Contig ID 266229_1.R1040
 5'-most EST uC-gmropic056g11b1
 Method BLASTX
 NCBI GI g629561
 BLAST score 248
 E value 4.0e-21
 Match length 121
 % identity 44
 NCBI Description SRG1 protein - Arabidopsis thaliana
 >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis
 thaliana]

Seq. No. 32058
 Contig ID 266238_1.R1040
 5'-most EST zsg701119112.h1

Seq. No. 32059
 Contig ID 266276_1.R1040
 5'-most EST gsv701054413.h1

Seq. No. 32060
 Contig ID 266280_1.R1040
 5'-most EST gsv701056418.h1
 Method BLASTX
 NCBI GI g3411152
 BLAST score 191
 E value 8.0e-15
 Match length 54
 % identity 69
 NCBI Description (AF066050) thymidine kinase [Oryza sativa]

Seq. No. 32061
 Contig ID 266337_1.R1040
 5'-most EST uC-gmrominsoy310d10b1
 Method BLASTX
 NCBI GI g3335373
 BLAST score 284
 E value 2.0e-25
 Match length 72
 % identity 71
 NCBI Description (AC003028) putative GTL1 protein [Arabidopsis thaliana]

Seq. No. 32062
 Contig ID 266337_2.R1040
 5'-most EST uC-gmrominsoy125a08b1
 Method BLASTX

NCBI GI g3335373
 BLAST score 385
 E value 3.0e-37
 Match length 93
 % identity 74
 NCBI Description (AC003028) putative GTL1 protein [Arabidopsis thaliana]

Seq. No. 32063
 Contig ID 266356_1.R1040
 5'-most EST uC-gmropic012d12b1
 Method BLASTX
 NCBI GI g1663541
 BLAST score 224
 E value 2.0e-18
 Match length 91
 % identity 58
 NCBI Description (U55805) disease resistance protein homolog [Glycine max]

Seq. No. 32064
 Contig ID 266428_1.R1040
 5'-most EST gsv701054626.h1

Seq. No. 32065
 Contig ID 266487_1.R1040
 5'-most EST jC-gmle01810018c01a2

Seq. No. 32066
 Contig ID 266605_1.R1040
 5'-most EST epx701109042.h1
 Method BLASTX
 NCBI GI g3242071
 BLAST score 285
 E value 3.0e-25
 Match length 163
 % identity 42
 NCBI Description (AJ007289) myb-like protein [Arabidopsis thaliana]

Seq. No. 32067
 Contig ID 266624_1.R1040
 5'-most EST gsv701055903.h1
 Method BLASTX
 NCBI GI g2827709
 BLAST score 446
 E value 2.0e-44
 Match length 114
 % identity 73
 NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

Seq. No. 32068
 Contig ID 266713_1.R1040
 5'-most EST gsv701055205.h1

Seq. No. 32069
 Contig ID 266809_1.R1040
 5'-most EST gsv701055203.h1
 Method BLASTN
 NCBI GI g28589

BLAST score 315
 E value 1.0e-177
 Match length 315
 % identity 100
 NCBI Description Human messenger RNA for serum albumin (HSA)

Seq. No. 32070
 Contig ID 266881_1.R1040
 5'-most EST uC-gmrominsoy219f09b1

Seq. No. 32071
 Contig ID 266882_1.R1040
 5'-most EST jC-gmle01810082f09a1
 Method BLASTX
 NCBI GI g4490316
 BLAST score 242
 E value 2.0e-20
 Match length 123
 % identity 43
 NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No. 32072
 Contig ID 266933_1.R1040
 5'-most EST gsv701055343.h1
 Method BLASTX
 NCBI GI g3551954
 BLAST score 176
 E value 1.0e-12
 Match length 78
 % identity 44
 NCBI Description (AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]

Seq. No. 32073
 Contig ID 267126_1.R1040
 5'-most EST gsv701055586.h1

Seq. No. 32074
 Contig ID 267154_1.R1040
 5'-most EST jC-gmfl02220103a08a1
 Method BLASTX
 NCBI GI g3510254
 BLAST score 148
 E value 2.0e-09
 Match length 41
 % identity 78
 NCBI Description (AC005310) putative zinc transporter [Arabidopsis thaliana]

Seq. No. 32075
 Contig ID 267155_1.R1040
 5'-most EST gsv701055657.h1

Seq. No. 32076
 Contig ID 267175_1.R1040
 5'-most EST uC-gmrominsoy072e01b1
 Method BLASTX
 NCBI GI g3334142

BLAST score 579
 E value 6.0e-60
 Match length 148
 % identity 76
 NCBI Description CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5
 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5)
 >gi_2737892 (U59150) nucleolar protein AfCbf5p [Sartorya
 fumigata]

Seq. No. 32077
 Contig ID 267306_1.R1040
 5'-most EST fC-gmro700763939d3
 Method BLASTX
 NCBI GI g3201554
 BLAST score 328
 E value 2.0e-30
 Match length 62
 % identity 95
 NCBI Description (AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No. 32078
 Contig ID 267411_1.R1040
 5'-most EST gsv701055941.h1
 Method BLASTX
 NCBI GI g3688284
 BLAST score 595
 E value 8.0e-62
 Match length 146
 % identity 73
 NCBI Description (AJ011567) lanatoside 15'-O-acetylerase [Digitalis
 lanata]

Seq. No. 32079
 Contig ID 267480_1.R1040
 5'-most EST jC-gmro02910003g06a1

Seq. No. 32080
 Contig ID 267608_1.R1040
 5'-most EST jC-gmro02910061c08a1
 Method BLASTX
 NCBI GI g1857447
 BLAST score 251
 E value 1.0e-21
 Match length 110
 % identity 47
 NCBI Description (U82367) UDP-glucose glucosyltransferase [Solanum
 tuberosum]

Seq. No. 32081
 Contig ID 267784_1.R1040
 5'-most EST zsg701126354.h1
 Method BLASTX
 NCBI GI g4388832
 BLAST score 514
 E value 2.0e-52
 Match length 119
 % identity 85

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NCBI Description (AC006528) putative DNA replication licensing factor with an MCM family domain (prosite:PDOC00662) [Arabidopsis thaliana]

Seq. No. 32082
Contig ID 267856_1.R1040
5'-most EST epX701108984.h1

Seq. No. 32083
Contig ID 267885_1.R1040
5'-most EST gsv701056530.h1
Method BLASTX
NCBI GI g3176671
BLAST score 227
E value 7.0e-19
Match length 69
% identity 59

NCBI Description (AC004393) Contains similarity to hypothetical gene B0495.7 gb_687822 from C. elegans cosmid gb_U21317. [Arabidopsis thaliana]

Seq. No. 32084
Contig ID 267894_1.R1040
5'-most EST gsv701056543.h1

Seq. No. 32085
Contig ID 267922_1.R1040
5'-most EST epX701107501.h1

Seq. No. 32086
Contig ID 267929_1.R1040
5'-most EST jC-gmro02910048c01a1
Method BLASTX
NCBI GI g1346396
BLAST score 150
E value 1.0e-09
Match length 85
% identity 35

NCBI Description PUTATIVE RECEPTOR PROTEIN KINASE ZMPK1 PRECURSOR
>gi_100913_pir_S10930 probable receptor protein kinase (EC 2.7.1.-) precursor - maize >gi_22432_emb_CAA36611_ (X52384) precursor protein (AA -26 to 791) [Zea mays]
>gi_22436_emb_CAA47962_ (X67733) receptor-like protein kinase [Zea mays] >gi_226927_prf_1611404A receptor protein kinase [Zea mays]

Seq. No. 32087
Contig ID 267936_1.R1040
5'-most EST gsv701056591.h1

Seq. No. 32088
Contig ID 267989_1.R1040
5'-most EST gsv701056662.h1

Seq. No. 32089
Contig ID 268024_1.R1040
5'-most EST gsv701056810.h1

NCBI GI	g2911276
BLAST score	138
E value	1.0e-08
Match length	64
% identity	45
NCBI Description	(U63631) LMW heat shock protein [Fragaria x ananassa]
Seq. No.	32097
Contig ID	268351_1.R1040
5'-most EST	uC-gmrominsoyl36g04b1
Seq. No.	32098
Contig ID	268417_1.R1040
5'-most EST	hrw701057018.h2
Seq. No.	32099
Contig ID	268438_1.R1040
5'-most EST	hrw701057058.h2
Seq. No.	32100
Contig ID	268504_1.R1040
5'-most EST	hrw701057302.h1
Method	BLASTN
NCBI GI	g1620016
BLAST score	189
E value	1.0e-102
Match length	205
% identity	98
NCBI Description	Human heart mRNA for heat shock protein 90, partial cds
Seq. No.	32101
Contig ID	268521_1.R1040
5'-most EST	hrw701057327.h1
Method	BLASTN
NCBI GI	g34200
BLAST score	252
E value	1.0e-140
Match length	272
% identity	98
NCBI Description	Human mRNA for ribosomal protein L35a >gi_4506638_ref_NM_000996.1_RPL35A_Homo sapiens ribosomal protein L35a (RPL35A) mRNA
Seq. No.	32102
Contig ID	268533_1.R1040
5'-most EST	hrw701057518.h1
Method	BLASTN
NCBI GI	g28338
BLAST score	446
E value	0.0e+00
Match length	545
% identity	96
NCBI Description	Human mRNA for cytoskeletal gamma-actin >gi_4501886_ref_NM_001614.1_ACTG1_Homo sapiens actin, gamma 1 (ACTG1) mRNA
Seq. No.	32103

NCBI Description Human mitochondrial specific single stranded DNA binding protein mRNA, complete cds.
 >gi_4507230_ref_NM_003143.1_SSBP_Homo sapiens
 single-stranded DNA-binding protein (SSBP), nuclear gene encoding mitochondrial protein, mRNA

Seq. No. 32108
 Contig ID 268642_1.R1040
 5'-most EST jC-gmle01810072a01d1
 Method BLASTN
 NCBI GI g1857236
 BLAST score 393
 E value 0.0e+00
 Match length 505
 % identity 94

NCBI Description Human p97 mRNA, complete cds
 >gi_4503538_ref_NM_001418.1 EIF4G2_Homo sapiens eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2) mRNA

Seq. No. 32109
 Contig ID 268644_1.R1040
 5'-most EST hrw701057542.h1
 Method BLASTN
 NCBI GI g4500180
 BLAST score 248
 E value 1.0e-137
 Match length 264
 % identity 98

NCBI Description Homo sapiens mRNA; cDNA DKFZp586N0318 (from clone DKFZp586N0318)

Seq. No. 32110
 Contig ID 268682_1.R1040
 5'-most EST zsg701129177.h1
 Method BLASTN
 NCBI GI g23690
 BLAST score 339
 E value 0.0e+00
 Match length 339
 % identity 100

NCBI Description H.sapiens mRNA for 23 kD highly basic protein

Seq. No. 32111
 Contig ID 268684_1.R1040
 5'-most EST hrw701057604.h1

Seq. No. 32112
 Contig ID 268692_1.R1040
 5'-most EST jC-gmf102220073e01a1

Seq. No. 32113
 Contig ID 268708_1.R1040
 5'-most EST kl1701212504.h1
 Method BLASTX
 NCBI GI g1076315
 BLAST score 361
 E value 1.0e-34

Match length 113
 % identity 70
 NCBI Description cytochrome P450 - Arabidopsis thaliana
 >gi_853719_emb_CAA60793_ (X87367) CYP90 protein
 [Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368)
 CYP90 protein [Arabidopsis thaliana]

Seq. No. 32114
 Contig ID 268869_1.R1040
 5'-most EST hrw701057915.h1
 Method BLASTX
 NCBI GI g2245006
 BLAST score 155
 E value 1.0e-10
 Match length 83
 % identity 45
 NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32115
 Contig ID 268870_1.R1040
 5'-most EST uC-gmrominsoy276d09b1

Seq. No. 32116
 Contig ID 268950_1.R1040
 5'-most EST hrw701058033.h1

Seq. No. 32117
 Contig ID 268983_1.R1040
 5'-most EST hrw701058092.h1
 Method BLASTN
 NCBI GI g1370187
 BLAST score 230
 E value 1.0e-126
 Match length 354
 % identity 92
 NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB7D

Seq. No. 32118
 Contig ID 269005_1.R1040
 5'-most EST hrw701058205.h1
 Method BLASTX
 NCBI GI g2618684
 BLAST score 183
 E value 8.0e-14
 Match length 61
 % identity 57
 NCBI Description (AC002510) putative
 UDP-N-acetylglucosamine--dolichyl-phosphate
 N-acetylglucosaminephosphotransferase [Arabidopsis
 thaliana] >gi_3241947 (AC004625) putative
 UDP-N-acetylglucosamine--dolichyl-phosphate
 N-acetylglucosaminephosphotransferase [Arabidopsis
 thaliana]

Seq. No. 32119
 Contig ID 269092_1.R1040
 5'-most EST hrw701058318.h1

Method BLASTX
 NCBI GI g2342719
 BLAST score 141
 E value 6.0e-09
 Match length 87
 % identity 39
 NCBI Description (AC002341) SF16 protein isolog [Arabidopsis thaliana]

Seq. No. 32120
 Contig ID 269096_1.R1040
 5'-most EST hrw701058333.h1

Seq. No. 32121
 Contig ID 269119_1.R1040
 5'-most EST jsh701068477.h1

Seq. No. 32122
 Contig ID 269197_1.R1040
 5'-most EST hrw701058652.h1

Seq. No. 32123
 Contig ID 269250_1.R1040
 5'-most EST jC-gmro02910051e04d1
 Method BLASTX
 NCBI GI g3549660
 BLAST score 332
 E value 9.0e-31
 Match length 108
 % identity 55
 NCBI Description (AL031394) carbonate dehydratase - like protein [Arabidopsis thaliana]

Seq. No. 32124
 Contig ID 269268_1.R1040
 5'-most EST g5057717

Seq. No. 32125
 Contig ID 269308_1.R1040
 5'-most EST hrw701058718.h1
 Method BLASTX
 NCBI GI g3135269
 BLAST score 252
 E value 2.0e-21
 Match length 159
 % identity 45
 NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]

Seq. No. 32126
 Contig ID 269373_1.R1040
 5'-most EST hrw701061721.h1
 Method BLASTX
 NCBI GI g1769556
 BLAST score 415
 E value 6.0e-41
 Match length 101
 % identity 81
 NCBI Description (U81158) Forsythia x intermedia

Method BLASTX
 NCBI GI g4220515
 BLAST score 451
 E value 6.0e-45
 Match length 153
 % identity 57
 NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 32139
 Contig ID 269695_1.R1040
 5'-most EST uC-gmflminsoy080h10b1
 Method BLASTX
 NCBI GI g2832629
 BLAST score 349
 E value 2.0e-32
 Match length 251
 % identity 37
 NCBI Description (AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]

Seq. No. 32140
 Contig ID 269751_1.R1040
 5'-most EST jsh701069189.h1
 Method BLASTX
 NCBI GI g2244910
 BLAST score 144
 E value 1.0e-09
 Match length 52
 % identity 46
 NCBI Description (Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No. 32141
 Contig ID 269824_1.R1040
 5'-most EST jsh701064879.h1
 Method BLASTX
 NCBI GI g101065
 BLAST score 139
 E value 1.0e-08
 Match length 95
 % identity 32
 NCBI Description rad4 protein - fission yeast (Schizosaccharomyces pombe)

Seq. No. 32142
 Contig ID 269837_1.R1040
 5'-most EST hrw701059564.h1
 Method BLASTX
 NCBI GI g4249385
 BLAST score 247
 E value 2.0e-21
 Match length 67
 % identity 66
 NCBI Description (AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No. 32143
 Contig ID 269879_1.R1040
 5'-most EST hrw701059615.h1

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5'-most EST hrw701060856.h1
 Method BLASTX
 NCBI GI g3128210
 BLAST score 183
 E value 7.0e-14
 Match length 56
 % identity 68
 NCBI Description (AC004077) putative cytochrome P450 protein [Arabidopsis thaliana] >gi_3337378 (AC004481) putative cytochrome P450 protein [Arabidopsis thaliana]

Seq. No. 32158
 Contig ID 270990_1.R1040
 5'-most EST uC-gmrominsoy0001b04a1

Seq. No. 32159
 Contig ID 271051_1.R1040
 5'-most EST asn701137356.h1
 Method BLASTX
 NCBI GI g4522004
 BLAST score 190
 E value 1.0e-14
 Match length 53
 % identity 70
 NCBI Description (AC007069) putative histidine kinase, sensory transduction [Arabidopsis thaliana]

Seq. No. 32160
 Contig ID 271120_1.R1040
 5'-most EST hrw701061322.h1

Seq. No. 32161
 Contig ID 271141_1.R1040
 5'-most EST hrw701061352.h1

Seq. No. 32162
 Contig ID 271153_1.R1040
 5'-most EST hrw701061372.h1
 Method BLASTX
 NCBI GI g3068704
 BLAST score 414
 E value 9.0e-41
 Match length 118
 % identity 66
 NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No. 32163
 Contig ID 271235_1.R1040
 5'-most EST hrw701061486.h1

Seq. No. 32164
 Contig ID 271286_1.R1040
 5'-most EST k11701202348.h1
 Method BLASTX
 NCBI GI g119095
 BLAST score 187
 E value 2.0e-14

Seq. No. 32187
 Contig ID 272325_1.R1040
 5'-most EST hrw701063082.h1
 Method BLASTX
 NCBI GI g3047096
 BLAST score 585
 E value 1.0e-60
 Match length 143
 % identity 77
 NCBI Description (AF058826) similar to eukaryotic protein kinase domains
 (Pfam: pkinase.hmm, score: 189.74) [Arabidopsis thaliana]

Seq. No. 32188
 Contig ID 272377_1.R1040
 5'-most EST jC-gmro02910065c08d1
 Method BLASTX
 NCBI GI g1370174
 BLAST score 271
 E value 9.0e-24
 Match length 63
 % identity 79
 NCBI Description (Z73936) RAB1Y [Lotus japonicus]

Seq. No. 32189
 Contig ID 272394_1.R1040
 5'-most EST jC-gmst02400077h05d1
 Method BLASTX
 NCBI GI g3395432
 BLAST score 286
 E value 1.0e-25
 Match length 63
 % identity 83
 NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 32190
 Contig ID 272486_1.R1040
 5'-most EST hrw701063284.h1

Seq. No. 32191
 Contig ID 272534_2.R1040
 5'-most EST kl1701211827.h1
 Method BLASTX
 NCBI GI g3337367
 BLAST score 128
 E value 6.0e-17
 Match length 77
 % identity 61
 NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32192
 Contig ID 272641_1.R1040
 5'-most EST jsh701065193.h1

Seq. No. 32193
 Contig ID 272710_1.R1040
 5'-most EST hrw701063586.h1
 Method BLASTX

0984016 103000

Seq. No. 32201
 Contig ID 273183_1.R1040
 5'-most EST jsh701064044.h1
 Method BLASTX
 NCBI GI g571484
 BLAST score 359
 E value 1.0e-34
 Match length 84
 % identity 85
 NCBI Description (U16727) peroxidase precursor [Medicago truncatula]

Seq. No. 32202
 Contig ID 273229_1.R1040
 5'-most EST jsh701064102.h1
 Method BLASTX
 NCBI GI g3201541
 BLAST score 148
 E value 9.0e-10
 Match length 31
 % identity 77
 NCBI Description (AJ005077) TCTR2 protein [Lycopersicon esculentum]

Seq. No. 32203
 Contig ID 273375_1.R1040
 5'-most EST jsh701065331.h1

Seq. No. 32204
 Contig ID 273443_1.R1040
 5'-most EST uC-gmflminsoy010c03b1

Seq. No. 32205
 Contig ID 273451_2.R1040
 5'-most EST jsh701065694.h1
 Method BLASTX
 NCBI GI g4262173
 BLAST score 211
 E value 3.0e-17
 Match length 82
 % identity 59
 NCBI Description (AC005508) 3975 [Arabidopsis thaliana]

Seq. No. 32206
 Contig ID 273492_1.R1040
 5'-most EST jC-gmfl02220068d02a1

Seq. No. 32207
 Contig ID 273547_1.R1040
 5'-most EST jC-gmfl02220050f07d1

Seq. No. 32208
 Contig ID 273621_1.R1040
 5'-most EST zsg701125691.h1

Seq. No. 32209
 Contig ID 273637_1.R1040
 5'-most EST g5508930

000101 91048960

5'-most EST	jC-gmle01810044b10a1
Seq. No.	32226
Contig ID	274480_1.R1040
5'-most EST	jsh701065988.h1
Method	BLASTX
NCBI GI	g3184285
BLAST score	178
E value	9.0e-13
Match length	78
% identity	41
NCBI Description	(AC004136) hypothetical protein [Arabidopsis thaliana]
Seq. No.	32227
Contig ID	274535_1.R1040
5'-most EST	kwa701015687.h1
Seq. No.	32228
Contig ID	274623_1.R1040
5'-most EST	jsh701066228.h1
Method	BLASTX
NCBI GI	g2244732
BLAST score	185
E value	9.0e-14
Match length	69
% identity	48
NCBI Description	(D88413) endo-xyloglucan transferase [Gossypium hirsutum]
Seq. No.	32229
Contig ID	274653_1.R1040
5'-most EST	jsh701066272.h1
Seq. No.	32230
Contig ID	274795_1.R1040
5'-most EST	jC-gmro02910072c05a1
Seq. No.	32231
Contig ID	274810_1.R1040
5'-most EST	jC-gmro02910070b12a1
Seq. No.	32232
Contig ID	274867_1.R1040
5'-most EST	jsh701066587.h1
Seq. No.	32233
Contig ID	274955_1.R1040
5'-most EST	zsg701118382.h1
Method	BLASTX
NCBI GI	g2252632
BLAST score	339
E value	6.0e-32
Match length	92
% identity	64
NCBI Description	(U95973) Barley Mlo protein isolog [Arabidopsis thaliana]
Seq. No.	32234
Contig ID	274968_1.R1040

5'-most EST jC-gmle01810091f09a1
 Method BLASTX
 NCBI GI g2864618
 BLAST score 231
 E value 3.0e-19
 Match length 85
 % identity 53
 NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 32235
 Contig ID 275067_1.R1040
 5'-most EST jsh701066875.h1

Seq. No. 32236
 Contig ID 275072_1.R1040
 5'-most EST jC-gmle01810043a10a1
 Method BLASTX
 NCBI GI g3096947
 BLAST score 186
 E value 8.0e-14
 Match length 83
 % identity 54
 NCBI Description (Y16327) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]

Seq. No. 32237
 Contig ID 275094_1.R1040
 5'-most EST jsh701066921.h1

Seq. No. 32238
 Contig ID 275196_1.R1040
 5'-most EST jsh701067139.h1

Seq. No. 32239
 Contig ID 275270_1.R1040
 5'-most EST zsg701122675.h1
 Method BLASTX
 NCBI GI g3281868
 BLAST score 216
 E value 9.0e-18
 Match length 48
 % identity 92
 NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 32240
 Contig ID 275366_1.R1040
 5'-most EST fC-gmse700754068d2
 Method BLASTX
 NCBI GI g3785996
 BLAST score 334
 E value 1.0e-35
 Match length 125
 % identity 41
 NCBI Description (AC005499) putative annexin [Arabidopsis thaliana]

Seq. No. 32241
 Contig ID 275367_1.R1040

5'-most EST uC-gmflminsoy072f04b1
Method BLASTX
NCBI GI g3367571
BLAST score 360
E value 3.0e-34
Match length 116
% identity 61
NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 32242
Contig ID 275435_1.R1040
5'-most EST jsh701067638.h1

Seq. No. 32243
Contig ID 275456_1.R1040
5'-most EST jsh701067739.h1

Seq. No. 32244
Contig ID 275490_1.R1040
5'-most EST jsh701068418.h1

Seq. No. 32245
Contig ID 275579_1.R1040
5'-most EST jC-gmf102220054f05d1
Method BLASTX
NCBI GI g1946355
BLAST score 171
E value 4.0e-12
Match length 88
% identity 42
NCBI Description (U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No. 32246
Contig ID 275588_1.R1040
5'-most EST uC-gmflminsoy064g11b1
Method BLASTX
NCBI GI g3452263
BLAST score 734
E value 4.0e-78
Match length 150
% identity 91
NCBI Description (AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis thaliana]

Seq. No. 32247
Contig ID 275600_1.R1040
5'-most EST jC-gmro02910023f06d1
Method BLASTX
NCBI GI g4240122
BLAST score 291
E value 2.0e-26
Match length 89
% identity 53
NCBI Description (AB007802) cytochrome b5 [Arabidopsis thaliana]

Seq. No.	32248
Contig ID	275623_1.R1040
5'-most EST	jC-gmro02910064c02a1
Method	BLASTX
NCBI GI	g1082054
BLAST score	179
E value	4.0e-13
Match length	87
% identity	37
NCBI Description	(Z49859) copper transporter protein [Arabidopsis thaliana]
Seq. No.	32249
Contig ID	275677_1.R1040
5'-most EST	jC-gmro02910019d06d1
Seq. No.	32250
Contig ID	275689_1.R1040
5'-most EST	jsh701068243.h1
Method	BLASTX
NCBI GI	g1575699
BLAST score	541
E value	1.0e-55
Match length	125
% identity	82
NCBI Description	(U70478) putative leucoanthocyanidin dioxygenase [Arabidopsis thaliana] >gi_3292813_emb_CAA19803 (AL031018) putative leucoanthocyanidin dioxygenase (LDOX) [Arabidopsis thaliana]
Seq. No.	32251
Contig ID	275701_1.R1040
5'-most EST	jsh701068263.h1
Method	BLASTX
NCBI GI	g2129854
BLAST score	178
E value	2.0e-14
Match length	63
% identity	57
NCBI Description	early nodulin 8 precursor - alfalfa >gi_304037 (L18899) early nodulin [Medicago sativa]
Seq. No.	32252
Contig ID	275895_1.R1040
5'-most EST	jsh701068541.h1
Seq. No.	32253
Contig ID	275898_1.R1040
5'-most EST	zsg701121326.h1
Method	BLASTN
NCBI GI	g2618600
BLAST score	37
E value	2.0e-11
Match length	41
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana]

Seq. No. 32254
 Contig ID 276134_1.R1040
 5'-most EST jsh701068942.h1
 Method BLASTX
 NCBI GI g2435406
 BLAST score 284
 E value 2.0e-25
 Match length 123
 % identity 53
 NCBI Description (U83490) thaumatin-like protein [Arabidopsis thaliana]

Seq. No. 32255
 Contig ID 276694_1.R1040
 5'-most EST jsh701069816.h1
 Method BLASTX
 NCBI GI g4218120
 BLAST score 326
 E value 4.0e-30
 Match length 75
 % identity 77
 NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No. 32256
 Contig ID 276694_2.R1040
 5'-most EST jC-gmst02400006g10d1
 Method BLASTX
 NCBI GI g4218120
 BLAST score 371
 E value 1.0e-35
 Match length 92
 % identity 72
 NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No. 32257
 Contig ID 276713_1.R1040
 5'-most EST g5605703
 Method BLASTX
 NCBI GI g3341694
 BLAST score 244
 E value 2.0e-20
 Match length 116
 % identity 44
 NCBI Description (AC003672) PREG-like protein [Arabidopsis thaliana]

Seq. No. 32258
 Contig ID 276867_1.R1040
 5'-most EST jsh701070084.h2
 Method BLASTX
 NCBI GI g746487
 BLAST score 185
 E value 8.0e-14
 Match length 76
 % identity 45
 NCBI Description (U23514) No definition line found [Caenorhabditis elegans]

Seq. No. 32266
 Contig ID 277447_1.R1040
 5'-most EST kl1701213720.h1
 Method BLASTX
 NCBI GI g3859592
 BLAST score 267
 E value 1.0e-23
 Match length 73
 % identity 73
 NCBI Description (AF104919) contains similarity to expansins [Arabidopsis thaliana]

Seq. No. 32267
 Contig ID 277568_1.R1040
 5'-most EST kl1701207518.h1
 Method BLASTX
 NCBI GI g4056506
 BLAST score 140
 E value 9.0e-09
 Match length 75
 % identity 36
 NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 32268
 Contig ID 277591_1.R1040
 5'-most EST kl1701202657.h1
 Method BLASTX
 NCBI GI g1076274
 BLAST score 183
 E value 7.0e-14
 Match length 53
 % identity 62
 NCBI Description cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)

Seq. No. 32269
 Contig ID 277674_1.R1040
 5'-most EST kl1701202770.h1

Seq. No. 32270
 Contig ID 277677_1.R1040
 5'-most EST kl1701202774.h1

Seq. No. 32271
 Contig ID 277743_1.R1040
 5'-most EST kl1701202883.h1
 Method BLASTX
 NCBI GI g2191137
 BLAST score 290
 E value 2.0e-26
 Match length 77
 % identity 69
 NCBI Description (AF007269) similar to the GDSL family of lipolytic enzymes [Arabidopsis thaliana]

Seq. No. 32272
 Contig ID 277750_1.R1040

5'-most EST k11701202993.h1

Seq. No. 32273
Contig ID 277767_1.R1040
5'-most EST k11701202917.h1
Method BLASTX
NCBI GI g1669591
BLAST score 361
E value 9.0e-35
Match length 90
% identity 73
NCBI Description (D88742) O-methyltransferase [Glycyrrhiza echinata]

Seq. No. 32274
Contig ID 277777_1.R1040
5'-most EST k11701202933.h1
Method BLASTX
NCBI GI g3688284
BLAST score 232
E value 1.0e-19
Match length 89
% identity 51
NCBI Description (AJ011567) lanatoside 15'-O-acetylerase [Digitalis lanata]

Seq. No. 32275
Contig ID 277801_1.R1040
5'-most EST g5753444
Method BLASTX
NCBI GI g2832625
BLAST score 152
E value 1.0e-12
Match length 91
% identity 56
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 32276
Contig ID 277804_1.R1040
5'-most EST k11701205008.h1

Seq. No. 32277
Contig ID 277817_1.R1040
5'-most EST k11701209742.h1
Method BLASTX
NCBI GI g4056403
BLAST score 343
E value 3.0e-32
Match length 124
% identity 56
NCBI Description (AD001673) lipoxygenase [Persea americana]

Seq. No. 32278
Contig ID 277844_1.R1040
5'-most EST zsg701130384.h1

Seq. No. 32279
Contig ID 277877_1.R1040

5'-most EST k11701203134.h1

Seq. No. 32280
Contig ID 277878_1.R1040
5'-most EST k11701203123.h1

Seq. No. 32281
Contig ID 277893_1.R1040
5'-most EST k11701214961.h1

Seq. No. 32282
Contig ID 278003_1.R1040
5'-most EST k11701212941.h1

Seq. No. 32283
Contig ID 278011_1.R1040
5'-most EST uC-gmrominsoy066a05b1
Method BLASTX
NCBI GI g2262177
BLAST score 485
E value 1.0e-48
Match length 214
% identity 50
NCBI Description (AC002329) hypothetical protein similar to T18A10.3
[Arabidopsis thaliana]

Seq. No. 32284
Contig ID 278018_1.R1040
5'-most EST k11701203338.h1
Method BLASTX
NCBI GI g4204277
BLAST score 409
E value 3.0e-40
Match length 98
% identity 68
NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 32285
Contig ID 278040_1.R1040
5'-most EST jC-gmro02800043a11a1
Method BLASTX
NCBI GI g2655098
BLAST score 360
E value 3.0e-34
Match length 108
% identity 63
NCBI Description (AF023472) peptide transporter [Hordeum vulgare]

Seq. No. 32286
Contig ID 278093_1.R1040
5'-most EST k11701212102.h1
Method BLASTX
NCBI GI g4538930
BLAST score 306
E value 4.0e-28
Match length 99
% identity 63

NCBI Description (AL049483) putative peroxidase [Arabidopsis thaliana]

Seq. No. 32287
Contig ID 278112_1.R1040
5'-most EST uC-gmröpic093g12b1
Method BLASTX
NCBI GI g3548806
BLAST score 379
E value 2.0e-36
Match length 148
% identity 47

NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 32288
Contig ID 278116_1.R1040
5'-most EST jC-gmro02910071a12a1
Method BLASTX
NCBI GI g2262111
BLAST score 528
E value 8.0e-54
Match length 178
% identity 59

NCBI Description (AC002343) ribitol dehydrogenase isolog [Arabidopsis thaliana]

Seq. No. 32289
Contig ID 278120_1.R1040
5'-most EST k11701212133.h1

Seq. No. 32290
Contig ID 278124_1.R1040
5'-most EST k11701203501.h2

Seq. No. 32291
Contig ID 278157_1.R1040
5'-most EST uC-gmflminsoy057f04b1
Method BLASTX
NCBI GI g3201617
BLAST score 281
E value 6.0e-25
Match length 82
% identity 61

NCBI Description (AC004669) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32292
Contig ID 278162_1.R1040
5'-most EST k11701204108.h1
Method BLASTX
NCBI GI g2443890
BLAST score 221
E value 2.0e-18
Match length 52
% identity 73

NCBI Description (AC002294) similar to NAM (gp_X92205_1321924) and CUC2 (gp_AB002560_1944132) proteins [Arabidopsis thaliana]

Seq. No. 32293

[illegible]

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Seq. No.      32314
Contig ID     278811_1.R1040
5'-most EST  k11701204522.h2
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Method          BLASTX
NCBI GI         g4371292
BLAST score     167
E value        5.0e-12
Match length    69
% identity      54
NCBI Description (AC006260) unknown protein [Arabidopsis thaliana]

Seq. No.        32315
Contig ID       278862_1.R1040
5'-most EST     jC-gmr002910062f07d1

Seq. No.        32316
Contig ID       278940_1.R1040
5'-most EST     k11701204694.h1
Method          BLASTX
NCBI GI         g3269287
BLAST score     147
E value        3.0e-09
Match length    113
% identity      34
NCBI Description (AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No.        32317
Contig ID       278965_1.R1040
5'-most EST     uC-gmropic110c12b1

Seq. No.        32318
Contig ID       278999_1.R1040
5'-most EST     k11701204795.h1

Seq. No.        32319
Contig ID       279082_1.R1040
5'-most EST     k11701207154.h1
Method          BLASTX
NCBI GI         g529353
BLAST score     419
E value        8.0e-49
Match length    159
% identity      56
NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No.        32320
Contig ID       279116_1.R1040
5'-most EST     k11701204975.h1
Method          BLASTX
NCBI GI         g3426038
BLAST score     597
E value        6.0e-62
Match length    176
% identity      66
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.        32321
Contig ID       279440_1.R1040
5'-most EST     k11701205461.h1

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Contig ID 280837_1.R1040
 5'-most EST uC-gmflminsoy003c12b1
 Method BLASTX
 NCBI GI g4218011
 BLAST score 770
 E value 4.0e-82
 Match length 200
 % identity 72
 NCBI Description (AC006135) putative protein kinase [Arabidopsis thaliana]
 >gi_4309721_gb_AAD15491_ (AC006439) putative
 serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 32344
 Contig ID 280906_1.R1040
 5'-most EST uC-gmflminsoy109b08b1
 Method BLASTX
 NCBI GI g2133437
 BLAST score 219
 E value 7.0e-18
 Match length 100
 % identity 47
 NCBI Description RNA polymerase II second largest chain RPB2 - Euplotes
 octocarinatus (SGC9) >gi_2654279_emb_CAA47069_ (X66453)
 DNA-directed RNA polymerase [Euplotes octocarinatus]

Seq. No. 32345
 Contig ID 280913_1.R1040
 5'-most EST kl1701207655.h1
 Method BLASTX
 NCBI GI g3776559
 BLAST score 409
 E value 3.0e-40
 Match length 97
 % identity 77
 NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi_3482933
 cdc2 protein kinase homolog from A. thaliana BAC
 gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this
 gene. [Arabidopsis thaliana]

Seq. No. 32346
 Contig ID 280934_1.R1040
 5'-most EST epX701109379.h1

Seq. No. 32347
 Contig ID 280949_1.R1040
 5'-most EST kl1701207867.h1

Seq. No. 32348
 Contig ID 280958_1.R1040
 5'-most EST kl1701209323.h1
 Method BLASTX
 NCBI GI g3924597
 BLAST score 138
 E value 1.0e-08
 Match length 87
 % identity 37
 NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No. 32349
 Contig ID 281016_1.R1040
 5'-most EST jC-gmro02910004a10d1
 Method BLASTX
 NCBI GI g2244973
 BLAST score 413
 E value 3.0e-40
 Match length 193
 % identity 40
 NCBI Description (Z97340) similarity to extensin class 1 protein
 [Arabidopsis thaliana]

Seq. No. 32350
 Contig ID 281054_1.R1040
 5'-most EST k11701208323.h1
 Method BLASTX
 NCBI GI g2342735
 BLAST score 162
 E value 2.0e-11
 Match length 49
 % identity 67
 NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]

Seq. No. 32351
 Contig ID 281129_1.R1040
 5'-most EST k11701207975.h1

Seq. No. 32352
 Contig ID 281132_1.R1040
 5'-most EST jC-gmle01810018a08a2

Seq. No. 32353
 Contig ID 281150_1.R1040
 5'-most EST k11701208002.h1

Seq. No. 32354
 Contig ID 281183_1.R1040
 5'-most EST k11701208043.h1
 Method BLASTX
 NCBI GI g4204297
 BLAST score 519
 E value 6.0e-53
 Match length 106
 % identity 92
 NCBI Description (AC003027) ADK1 [Arabidopsis thaliana]

Seq. No. 32355
 Contig ID 281226_1.R1040
 5'-most EST k11701208104.h1
 Method BLASTX
 NCBI GI g3150412
 BLAST score 231
 E value 2.0e-19
 Match length 67
 % identity 66
 NCBI Description (AC004165) putative Fe(II) transport protein [Arabidopsis

thaliana] >gi_3420044 (AC004680) putative Fe(II) transport protein [Arabidopsis thaliana]

Seq. No. 32356
Contig ID 281256_1.R1040
5'-most EST kl1701208136.h1

Seq. No. 32357
Contig ID 281280_1.R1040
5'-most EST kl1701208165.h1

Seq. No. 32358
Contig ID 281382_1.R1040
5'-most EST uC-gmrominsoy154a05b1

Seq. No. 32359
Contig ID 281409_1.R1040
5'-most EST kl1701208332.h1

Seq. No. 32360
Contig ID 281441_1.R1040
5'-most EST kl1701208373.h1

Seq. No. 32361
Contig ID 281462_1.R1040
5'-most EST kl1701215446.h1

Seq. No. 32362
Contig ID 281545_1.R1040
5'-most EST uC-gmronoir030e01b1

Seq. No. 32363
Contig ID 281681_1.R1040
5'-most EST kl1701208708.h1

Seq. No. 32364
Contig ID 281683_1.R1040
5'-most EST kl1701212911.h1
Method BLASTX
NCBI GI g1619602
BLAST score 235
E value 7.0e-20
Match length 53
% identity 87
NCBI Description (Y08726) MtN3 [Medicago truncatula]

Seq. No. 32365
Contig ID 281705_1.R1040
5'-most EST kl1701208747.h1
Method BLASTX
NCBI GI g3115374
BLAST score 483
E value 1.0e-48
Match length 106
% identity 86
NCBI Description (AF002016) acyl CoA oxidase homolog [Cucurbita sp.]

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Seq. No. 32374
 Contig ID 281977_1.R1040
 5'-most EST k11701209177.h1

Seq. No. 32375
 Contig ID 282020_1.R1040
 5'-most EST k11701209233.h1

Seq. No. 32376
 Contig ID 282027_1.R1040
 5'-most EST k11701212080.h1

Seq. No. 32377
 Contig ID 282180_1.R1040
 5'-most EST k11701214205.h1

Seq. No. 32378
 Contig ID 282325_1.R1040
 5'-most EST k11701209656.h1

Seq. No. 32379
 Contig ID 282326_1.R1040
 5'-most EST g4293821
 Method BLASTX
 NCBI GI g2981463
 BLAST score 118
 E value 5.0e-09
 Match length 93
 % identity 34
 NCBI Description (AF052663) gamma-tubulin interacting protein [Xenopus laevis]

Seq. No. 32380
 Contig ID 282347_1.R1040
 5'-most EST asn701140632.h1
 Method BLASTX
 NCBI GI g4235430
 BLAST score 239
 E value 3.0e-20
 Match length 69
 % identity 68
 NCBI Description (AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No. 32381
 Contig ID 282379_1.R1040
 5'-most EST k11701214478.h1

Seq. No. 32382
 Contig ID 282402_1.R1040
 5'-most EST k11701213719.h1

Seq. No. 32383
 Contig ID 282420_1.R1040
 5'-most EST k11701213504.h1
 Method BLASTX
 NCBI GI g4220491
 BLAST score 202

>gi_4559383_gb_AAD23043.1_AC006526_8 (AC006526) putative
DNA binding protein CPC [Arabidopsis thaliana]

Seq. No. 32413
Contig ID 284077_1.R1040
5'-most EST jC-gmle01810050a05a1
Method BLASTX
NCBI GI g3355486
BLAST score 193
E value 6.0e-15
Match length 51
% identity 63
NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 32414
Contig ID 284124_1.R1040
5'-most EST kl1701212277.h1

Seq. No. 32415
Contig ID 284193_1.R1040
5'-most EST uC-gmrominsoy046e07b1

Seq. No. 32416
Contig ID 284214_1.R1040
5'-most EST kl1701212403.h1

Seq. No. 32417
Contig ID 284244_1.R1040
5'-most EST kl1701212684.h1
Method BLASTX
NCBI GI g3885329
BLAST score 339
E value 3.0e-32
Match length 78
% identity 82
NCBI Description (AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No. 32418
Contig ID 284423_1.R1040
5'-most EST uC-gmflminsoy071a07b2

Seq. No. 32419
Contig ID 284428_1.R1040
5'-most EST asn701143228.h1

Seq. No. 32420
Contig ID 284450_1.R1040
5'-most EST jC-gmle01810054a10a1

Seq. No. 32421
Contig ID 284511_1.R1040
5'-most EST epx701107757.h1

Seq. No. 32422
Contig ID 284560_1.R1040
5'-most EST uC-gmflminsoy025c12b1
Method BLASTX

NCBI GI g2352492
 BLAST score 520
 E value 7.0e-53
 Match length 125
 % identity 75
 NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No. 32423
 Contig ID 284660_1.R1040
 5'-most EST epx701108257.h1

Seq. No. 32424
 Contig ID 284705_1.R1040
 5'-most EST epx701109068.h1

Seq. No. 32425
 Contig ID 284768_1.R1040
 5'-most EST uC-gmflminsoy007b12b1

Seq. No. 32426
 Contig ID 284798_1.R1040
 5'-most EST jC-gmro02910039h06a1

Seq. No. 32427
 Contig ID 284824_1.R1040
 5'-most EST kl1701213216.h1

Seq. No. 32428
 Contig ID 284855_1.R1040
 5'-most EST zsg701121725.h1

Seq. No. 32429
 Contig ID 284880_1.R1040
 5'-most EST jC-gmro02910050e09d1

Seq. No. 32430
 Contig ID 284889_1.R1040
 5'-most EST jC-gmfl02220092d01a1

Seq. No. 32431
 Contig ID 285001_1.R1040
 5'-most EST uC-gmrominsoy033d10b1
 Method BLASTX
 NCBI GI g2459412
 BLAST score 172
 E value 6.0e-12
 Match length 103
 % identity 43
 NCBI Description (AC002332) putative G9a protein [Arabidopsis thaliana]

Seq. No. 32432
 Contig ID 285042_1.R1040
 5'-most EST jC-gmro02910002a07a1

Seq. No. 32433

Contig ID 285049 1.R1040
 5'-most EST g5509313
 Method BLASTX
 NCBI GI g2864625
 BLAST score 320
 E value 2.0e-29
 Match length 92
 % identity 67
 NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 32434
 Contig ID 285172 1.R1040
 5'-most EST kl1701213667.h1

Seq. No. 32435
 Contig ID 285185 2.R1040
 5'-most EST jC-gmst02400066b03d1

Seq. No. 32436
 Contig ID 285304 1.R1040
 5'-most EST uC-gmröpic015d09b1
 Method BLASTN
 NCBI GI g3869068
 BLAST score 64
 E value 3.0e-27
 Match length 300
 % identity 80
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No. 32437
 Contig ID 285340 1.R1040
 5'-most EST kl1701213890.h1
 Method BLASTX
 NCBI GI g2569940
 BLAST score 264
 E value 1.0e-27
 Match length 136
 % identity 50
 NCBI Description (Y15194) GRS protein [Arabidopsis thaliana]

Seq. No. 32438
 Contig ID 285365 1.R1040
 5'-most EST zsg701122787.h1

Seq. No. 32439
 Contig ID 285400 1.R1040
 5'-most EST zsg701125845.h1

Seq. No. 32440
 Contig ID 285447 1.R1040
 5'-most EST kl1701214043.h1
 Method BLASTX
 NCBI GI g2160166
 BLAST score 288
 E value 4.0e-26
 Match length 94

Seq. No. 32447
 Contig ID 285827_1.R1040
 5'-most EST uC-gmröpic017h02b1
 Method BLASTX
 NCBI GI g1076758
 BLAST score 528
 E value 6.0e-54
 Match length 131
 % identity 76
 NCBI Description heat-shock protein precursor - rye >gi_2130093_pir__S65776
 heat-shock protein, 82K, precursor - rye
 >gi_556673_emb_CAA82945_ (Z30243) heat-shock protein
 [Secale cereale]

Seq. No. 32448
 Contig ID 285852_1.R1040
 5'-most EST kl1701214562.h1
 Method BLASTX
 NCBI GI g4151319
 BLAST score 147
 E value 1.0e-09
 Match length 30
 % identity 93
 NCBI Description (AF089084) putative auxin efflux carrier protein; AtPIN1
 [Arabidopsis thaliana]

Seq. No. 32449
 Contig ID 285872_1.R1040
 5'-most EST kl1701214554.h1

Seq. No. 32450
 Contig ID 285905_1.R1040
 5'-most EST uC-gmflminsoy072d01b1
 Method BLASTX
 NCBI GI g3763934
 BLAST score 230
 E value 4.0e-19
 Match length 109
 % identity 47
 NCBI Description (AC004450) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32451
 Contig ID 285926_1.R1040
 5'-most EST kl1701214620.h1
 Method BLASTX
 NCBI GI g2827637
 BLAST score 200
 E value 3.0e-15
 Match length 185
 % identity 30
 NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 32452
 Contig ID 285927_1.R1040
 5'-most EST kl1701215491.h1

Seq. No. 32453

Contig ID 285962_1.R1040
 5'-most EST jC-gmfl02220050g02a1
 Method BLASTX
 NCBI GI g3786000
 BLAST score 262
 E value 1.0e-22
 Match length 108
 % identity 45
 NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32454
 Contig ID 286210_1.R1040
 5'-most EST kl1701214989.h1
 Method BLASTX
 NCBI GI g3142303
 BLAST score 161
 E value 3.0e-11
 Match length 88
 % identity 39
 NCBI Description (AC002411) Strong similarity to MRP-like ABC transporter gb_U92650 from A. thaliana and canalicular multi-drug resistance protein gb_L49379 from Rattus norvegicus. [Arabidopsis thaliana]

Seq. No. 32455
 Contig ID 286282_1.R1040
 5'-most EST kl1701215347.h1

Seq. No. 32456
 Contig ID 286323_1.R1040
 5'-most EST kl1701215149.h1

Seq. No. 32457
 Contig ID 286343_1.R1040
 5'-most EST kl1701215175.h1

Seq. No. 32458
 Contig ID 286388_1.R1040
 5'-most EST kl1701215237.h1
 Method BLASTX
 NCBI GI g3738324
 BLAST score 237
 E value 3.0e-20
 Match length 88
 % identity 50
 NCBI Description (AC005170) GMP synthase-like protein [Arabidopsis thaliana]

Seq. No. 32459
 Contig ID 286478_1.R1040
 5'-most EST g5605942

Seq. No. 32460
 Contig ID 286527_1.R1040
 5'-most EST asn701139270.h1

Seq. No. 32461
 Contig ID 286548_1.R1040

5'-most EST k11701215463.h1
 Method BLASTX
 NCBI GI g4544473
 BLAST score 263
 E value 3.0e-23
 Match length 71
 % identity 39
 NCBI Description (AC006580) putative mei2 protein [Arabidopsis thaliana]

Seq. No. 32462
 Contig ID 286554_1.R1040
 5'-most EST k11701215470.h1
 Method BLASTX
 NCBI GI g1174718
 BLAST score 381
 E value 2.0e-36
 Match length 93
 % identity 78
 NCBI Description PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR
 >gi_322579_pir_JQ1674 receptor protein kinase TMK1 (EC
 2.7.1.-) precursor - Arabidopsis thaliana >gi_166888
 (L00670) protein kinase [Arabidopsis thaliana]

Seq. No. 32463
 Contig ID 286584_1.R1040
 5'-most EST epX701108777.h1

Seq. No. 32464
 Contig ID 286651_1.R1040
 5'-most EST epX701103856.h1

Seq. No. 32465
 Contig ID 286661_1.R1040
 5'-most EST epX701105166.h1

Seq. No. 32466
 Contig ID 286670_1.R1040
 5'-most EST asn701137942.h1
 Method BLASTX
 NCBI GI g2979558
 BLAST score 148
 E value 8.0e-10
 Match length 38
 % identity 74
 NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32467
 Contig ID 286690_1.R1040
 5'-most EST epX701103939.h1

Seq. No. 32468
 Contig ID 286748_1.R1040
 5'-most EST epX701104058.h1
 Method BLASTX
 NCBI GI g4049350
 BLAST score 217
 E value 2.0e-17

E value 8.0e-25
 Match length 87
 % identity 57
 NCBI Description (AJ007450) auxilin-like protein [Arabidopsis thaliana]

Seq. No. 32476
 Contig ID 287634_1.R1040
 5'-most EST jC-gmst02400067h03a1

Seq. No. 32477
 Contig ID 287636_1.R1040
 5'-most EST zsg701118226.h1

Seq. No. 32478
 Contig ID 287730_1.R1040
 5'-most EST zsg701118519.h1
 Method BLASTX
 NCBI GI g3805765
 BLAST score 564
 E value 6.0e-58
 Match length 156
 % identity 69
 NCBI Description (AC005693) putative protein kinase [Arabidopsis thaliana]

Seq. No. 32479
 Contig ID 287766_1.R1040
 5'-most EST epX701105492.h1

Seq. No. 32480
 Contig ID 287772_1.R1040
 5'-most EST jC-gmro02910059a04d1

Seq. No. 32481
 Contig ID 287868_1.R1040
 5'-most EST epX701105637.h1
 Method BLASTX
 NCBI GI g4454459
 BLAST score 605
 E value 5.0e-63
 Match length 147
 % identity 79
 NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 32482
 Contig ID 287932_1.R1040
 5'-most EST jC-gmro02910009d05a1
 Method BLASTX
 NCBI GI g4544451
 BLAST score 622
 E value 5.0e-65
 Match length 147
 % identity 78
 NCBI Description (AC006592) unknown protein [Arabidopsis thaliana]

Seq. No. 32483
 Contig ID 287960_1.R1040
 5'-most EST uC-gmrominsoy028d03b1

Seq. No. 32484
Contig ID 288006_1.R1040
5'-most EST zsg701121033.h1

Seq. No. 32485
Contig ID 288048_1.R1040
5'-most EST epX701105890.h1

Seq. No. 32486
Contig ID 288051_1.R1040
5'-most EST epX701105893.h1
Method BLASTX
NCBI GI g4432814
BLAST score 397
E value 7.0e-39
Match length 103
% identity 73
NCBI Description (AC006593) unknown protein [Arabidopsis thaliana]

Seq. No. 32487
Contig ID 288190_1.R1040
5'-most EST epX701106079.h1

Seq. No. 32488
Contig ID 288200_1.R1040
5'-most EST jC-gmfl02220079a03a1
Method BLASTX
NCBI GI g2244753
BLAST score 450
E value 8.0e-45
Match length 118
% identity 69
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32489
Contig ID 288218_1.R1040
5'-most EST g5676843

Seq. No. 32490
Contig ID 288258_1.R1040
5'-most EST jC-gmfl02220081b07d1

Seq. No. 32491
Contig ID 288325_1.R1040
5'-most EST epX701106274.h1
Method BLASTX
NCBI GI g3914621
BLAST score 151
E value 8.0e-10
Match length 129
% identity 12
NCBI Description RAN GTPASE ACTIVATING PROTEIN 1 >gi_2062660 (U88155)
RanGTPase activating protein [Xenopus laevis]

Seq. No. 32492
Contig ID 288425_1.R1040

5'-most EST jC-gmle01810078c08a1
 Method BLASTN
 NCBI GI g169036
 BLAST score 46
 E value 7.0e-17
 Match length 70
 % identity 91
 NCBI Description Pisum sativum L. aldolase gene, 3' end cds

Seq. No. 32493
 Contig ID 288482_1.R1040
 5'-most EST jC-gmro02910002a06d1

Seq. No. 32494
 Contig ID 288502_1.R1040
 5'-most EST epx701106518.h1
 Method BLASTX
 NCBI GI g585084
 BLAST score 153
 E value 6.0e-10
 Match length 56
 % identity 57
 NCBI Description ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)
 >gi_543383_pir_S40780 translation elongation factor G,
 mitochondrial - rat >gi_310102 (L14684) elongation factor G
 [Rattus norvegicus]

Seq. No. 32495
 Contig ID 288655_1.R1040
 5'-most EST epx701106718.h1
 Method BLASTX
 NCBI GI g4559371
 BLAST score 160
 E value 8.0e-11
 Match length 58
 % identity 53
 NCBI Description (AC006585) putative peroxidase [Arabidopsis thaliana]

Seq. No. 32496
 Contig ID 288657_1.R1040
 5'-most EST epx701106822.h1
 Method BLASTX
 NCBI GI g3114573
 BLAST score 314
 E value 3.0e-29
 Match length 92
 % identity 66
 NCBI Description (AF019383) 1-deoxyxylulose-5-phosphate synthase [Mentha x
 piperita]

Seq. No. 32497
 Contig ID 288876_1.R1040
 5'-most EST epx701107014.h1

Seq. No. 32498
 Contig ID 289043_1.R1040
 5'-most EST uC-gmropic037d09b1

Contig ID	290367_1.R1040
5'-most EST	epx701109171.h1
Seq. No.	32519
Contig ID	290387_1.R1040
5'-most EST	uC-gmflminsoy081h06b1
Seq. No.	32520
Contig ID	290399_1.R1040
5'-most EST	epx701109213.h1
Seq. No.	32521
Contig ID	290538_1.R1040
5'-most EST	epx701109416.h1
Method	BLASTX
NCBI GI	g4164145
BLAST score	306
E value	7.0e-28
Match length	114
% identity	48
NCBI Description	(AB012205) gibberelin 3beta-hydroxylase [Lactuca sativa]
Seq. No.	32522
Contig ID	290570_1.R1040
5'-most EST	epx701109489.h1
Method	BLASTX
NCBI GI	g2289003
BLAST score	699
E value	7.0e-74
Match length	179
% identity	76
NCBI Description	(AC002335) membrane transporter D1 isolog [Arabidopsis thaliana]
Seq. No.	32523
Contig ID	290580_1.R1040
5'-most EST	jC-gmle01810025a06a1
Method	BLASTX
NCBI GI	g2961352
BLAST score	250
E value	3.0e-21
Match length	58
% identity	74
NCBI Description	(AL022140) putative protein [Arabidopsis thaliana]
Seq. No.	32524
Contig ID	290699_1.R1040
5'-most EST	epx701110431.h1
Seq. No.	32525
Contig ID	290758_1.R1040
5'-most EST	epx701109965.h1
Seq. No.	32526
Contig ID	290812_1.R1040
5'-most EST	uC-gmropic042c05b1

Seq. No. 32527
 Contig ID 290842_1.R1040
 5'-most EST jC-gmf102220054f08d1
 Method BLASTX
 NCBI GI g2129755
 BLAST score 433
 E value 7.0e-43
 Match length 103
 % identity 83
 NCBI Description tryptophan synthase (EC 4.2.1.20) alpha chain - Arabidopsis thaliana >gi_619753 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] >gi_1585768_prf_2201482A Trp synthase:SUBUNIT=alpha [Arabidopsis thaliana]

Seq. No. 32528
 Contig ID 290888_1.R1040
 5'-most EST jC-gmle01810030g01a2
 Method BLASTX
 NCBI GI g2062173
 BLAST score 502
 E value 3.0e-51
 Match length 103
 % identity 95
 NCBI Description (AC001645) cell division protein FtsH isolog [Arabidopsis thaliana]

Seq. No. 32529
 Contig ID 290900_1.R1040
 5'-most EST uC-gmrominsoy047c01b1

Seq. No. 32530
 Contig ID 291084_1.R1040
 5'-most EST g5058010

Seq. No. 32531
 Contig ID 291208_1.R1040
 5'-most EST jC-gmro02910041017a1
 Method BLASTX
 NCBI GI g4314358
 BLAST score 527
 E value 2.0e-53
 Match length 318
 % identity 42
 NCBI Description (AC006340) putative kinesin heavy chain protein [Arabidopsis thaliana]

Seq. No. 32532
 Contig ID 291237_1.R1040
 5'-most EST uC-gmrominsoy167h04b1
 Method BLASTX
 NCBI GI g2827549
 BLAST score 691
 E value 7.0e-73
 Match length 146
 % identity 89
 NCBI Description (AL021635) glycoprotein endopeptidase - like protein [Arabidopsis thaliana]

5'-most EST zsg701119966.h1
 Method BLASTX
 NCBI GI g544075
 BLAST score 542
 E value 1.0e-55
 Match length 148
 % identity 68
 NCBI Description COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)
 (P102) >gi_486768_pir_S35312 coatomer complex chain beta'
 - bovine >gi_312732_emb_CAA51285_ (X72756) beta prime cop
 [Bos taurus]

Seq. No. 32562
 Contig ID 293335_1.R1040
 5'-most EST zsg701120037.h1
 Method BLASTX
 NCBI GI g1171429
 BLAST score 668
 E value 2.0e-70
 Match length 138
 % identity 57
 NCBI Description (U44028) CKC [Arabidopsis thaliana]

Seq. No. 32563
 Contig ID 293394_1.R1040
 5'-most EST g5057754
 Method BLASTX
 NCBI GI g2959324
 BLAST score 245
 E value 1.0e-20
 Match length 61
 % identity 79
 NCBI Description (Y15224) Importin alpha-like protein [Arabidopsis thaliana]

Seq. No. 32564
 Contig ID 293453_1.R1040
 5'-most EST zsg701120212.h1
 Method BLASTX
 NCBI GI g3176723
 BLAST score 188
 E value 6.0e-17
 Match length 104
 % identity 46
 NCBI Description (AC002392) putative protein kinase [Arabidopsis thaliana]

Seq. No. 32565
 Contig ID 293526_1.R1040
 5'-most EST jC-gmst02400055h08a1

Seq. No. 32566
 Contig ID 293613_1.R1040
 5'-most EST jC-gmst02400058h07a1

Seq. No. 32567
 Contig ID 293725_1.R1040
 5'-most EST zsg701126009.h1

NCBI GI g3549626
 BLAST score 166
 E value 1.0e-11
 Match length 108
 % identity 41
 NCBI Description (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

Seq. No. 32602
 Contig ID 295278_1.R1040
 5'-most EST zsg701123256.h1
 Method BLASTX
 NCBI GI g2583120
 BLAST score 153
 E value 1.0e-09
 Match length 170
 % identity 15
 NCBI Description (AC002387) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 32603
 Contig ID 295335_1.R1040
 5'-most EST asn701140185.h1

Seq. No. 32604
 Contig ID 295367_1.R1040
 5'-most EST zsg701123470.h1

Seq. No. 32605
 Contig ID 295386_1.R1040
 5'-most EST zsg701123392.h1

Seq. No. 32606
 Contig ID 295405_1.R1040
 5'-most EST zsg701123417.h1

Seq. No. 32607
 Contig ID 295413_1.R1040
 5'-most EST jC-gmst02400039a12a1
 Method BLASTX
 NCBI GI g3107903
 BLAST score 257
 E value 5.0e-22
 Match length 65
 % identity 69
 NCBI Description (D83719) polycomb-like protein [Daucus carota]

Seq. No. 32608
 Contig ID 295471_1.R1040
 5'-most EST uC-gmropic021b08b1
 Method BLASTX
 NCBI GI g3980384
 BLAST score 259
 E value 3.0e-22
 Match length 124
 % identity 42
 NCBI Description (AC004561) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32609
Contig ID 295614_1.R1040
5'-most EST zsg701123679.h1

Seq. No. 32610
Contig ID 295641_1.R1040
5'-most EST zsg701123866.h1

Seq. No. 32611
Contig ID 295713_1.R1040
5'-most EST jC-gmst02400065h01d1
Method BLASTX
NCBI GI g1055162
BLAST score 194
E value 8.0e-15
Match length 130
% identity 38
NCBI Description (U40029) coded for by C. elegans cDNA yk16b1.3; coded for by C. elegans cDNA yk8g6.5; coded for by C. elegans cDNA yk8g6.3; coded for by C. elegans cDNA yk6d3.5; coded for by C. elegans cDNA yk6d3.3; coded for by C. elegans cDNA yk7e12.5; co

Seq. No. 32612
Contig ID 295725_1.R1040
5'-most EST zsg701123841.h1

Seq. No. 32613
Contig ID 295776_1.R1040
5'-most EST zsg701123912.h1

Seq. No. 32614
Contig ID 295821_1.R1040
5'-most EST asn701142424.h1
Method BLASTX
NCBI GI g4191786
BLAST score 225
E value 2.0e-18
Match length 52
% identity 87
NCBI Description (AC005917) unknown protein [Arabidopsis thaliana]

Seq. No. 32615
Contig ID 295846_1.R1040
5'-most EST zsg701124006.h1

Seq. No. 32616
Contig ID 295873_1.R1040
5'-most EST zsg701124036.h1

Seq. No. 32617
Contig ID 295891_1.R1040
5'-most EST jC-gmle01810044a06a1
Method BLASTX
NCBI GI g4263778
BLAST score 342
E value 4.0e-32

Contig ID	297000_1.R1040
5'-most EST	uC-gmflminsoy079g06b1
Seq. No.	32635
Contig ID	297192_1.R1040
5'-most EST	jC-gmle01810030h05a2
Seq. No.	32636
Contig ID	297261_1.R1040
5'-most EST	zsg701126236.h1
Seq. No.	32637
Contig ID	297333_1.R1040
5'-most EST	uC-gmrominsoy256d12b1
Method	BLASTX
NCBI GI	g4204302
BLAST score	143
E value	7.0e-09
Match length	41
% identity	66
NCBI Description	(AC003027) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	32638
Contig ID	297447_1.R1040
5'-most EST	uC-gmröpic012f02b1
Seq. No.	32639
Contig ID	297574_1.R1040
5'-most EST	jC-gmfl02220051a08a1
Method	BLASTX
NCBI GI	g4001805
BLAST score	130
E value	8.0e-12
Match length	122
% identity	36
NCBI Description	(AF041476) BAF53a [Mus musculus]
Seq. No.	32640
Contig ID	297593_1.R1040
5'-most EST	fC-gmro700561647w1
Method	BLASTX
NCBI GI	g4510406
BLAST score	373
E value	2.0e-35
Match length	110
% identity	66
NCBI Description	(AC006587) putative protein kinase [Arabidopsis thaliana]
Seq. No.	32641
Contig ID	297594_1.R1040
5'-most EST	jC-gmle01810090d01a1
Method	BLASTX
NCBI GI	g3157943
BLAST score	141
E value	1.0e-14
Match length	98
% identity	50

component - rat >gi_203113 (M77245) beta'-chain clathrin
associated protein complex AP-1 [Rattus norvegicus]

Seq. No. 32695
Contig ID 301114_1.R1040
5'-most EST asn701133063.h1
Method BLASTX
NCBI GI g542058
BLAST score 161
E value 3.0e-11
Match length 52
% identity 58
NCBI Description HSR203J protein - common tobacco >gi_444002_emb_CAA54393_
(X77136) HSR203J [Nicotiana tabacum]

Seq. No. 32696
Contig ID 301138_1.R1040
5'-most EST jC-gmro02910017g12a1
Method BLASTX
NCBI GI g3242728
BLAST score 321
E value 1.0e-29
Match length 152
% identity 44
NCBI Description (AC003040) unknown protein [Arabidopsis thaliana]

Seq. No. 32697
Contig ID 301157_1.R1040
5'-most EST uC-gmflminsoy080c03b1

Seq. No. 32698
Contig ID 301243_1.R1040
5'-most EST jC-gmro02910068b05a1
Method BLASTX
NCBI GI g3860008
BLAST score 361
E value 3.0e-34
Match length 152
% identity 47
NCBI Description (AF091085) unknown [Homo sapiens]

Seq. No. 32699
Contig ID 301343_1.R1040
5'-most EST asn701133624.h2

Seq. No. 32700
Contig ID 301346_1.R1040
5'-most EST asn701141925.h1
Method BLASTX
NCBI GI g2739168
BLAST score 260
E value 1.0e-22
Match length 119
% identity 38
NCBI Description (AF032386) aldose-1-epimerase-like protein [Nicotiana
tabacum]

thaliana]

Seq. No. 32730
 Contig ID 303579_1.R1040
 5'-most EST uC-gmropic024c03b1

Seq. No. 32731
 Contig ID 303593_1.R1040
 5'-most EST jC-gmle01810091d08a1
 Method BLASTX
 NCBI GI g3252806
 BLAST score 305
 E value 9.0e-28
 Match length 139
 % identity 45
 NCBI Description (AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32732
 Contig ID 303869_1.R1040
 5'-most EST jC-gmro02910016b06d1

Seq. No. 32733
 Contig ID 304041_1.R1040
 5'-most EST jC-gmf102220067a12a1

Seq. No. 32734
 Contig ID 304136_1.R1040
 5'-most EST uC-gmropic024d05b1
 Method BLASTX
 NCBI GI g4263718
 BLAST score 670
 E value 1.0e-70
 Match length 154
 % identity 80
 NCBI Description (AC006223) putative DNA topoisomerase III beta [Arabidopsis thaliana]

Seq. No. 32735
 Contig ID 304179_1.R1040
 5'-most EST jC-gmro02910001c02a1
 Method BLASTX
 NCBI GI g4512665
 BLAST score 181
 E value 3.0e-13
 Match length 53
 % identity 64
 NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]
 >gi_4544472_gb_AAD22379.1_AC006580_11 (AC006580) unknown protein [Arabidopsis thaliana]

Seq. No. 32736
 Contig ID 304211_1.R1040
 5'-most EST jC-gmst02400025f08a1

Seq. No. 32737
 Contig ID 304306_1.R1040
 5'-most EST g4396105

Method BLASTX
 NCBI GI g4262167
 BLAST score 509
 E value 1.0e-51
 Match length 116
 % identity 83
 NCBI Description (AC005275) putative LRR receptor-linked protein kinase
 [Arabidopsis thaliana]

Seq. No. 32746
 Contig ID 305156_1.R1040
 5'-most EST asn701140683.h1

Seq. No. 32747
 Contig ID 305323_1.R1040
 5'-most EST jC-gmro02910006c08a1
 Method BLASTN
 NCBI GI g347454
 BLAST score 80
 E value 6.0e-37
 Match length 237
 % identity 40
 NCBI Description Soybean hydroxyproline-rich glycoprotein (sbHRGP2) mRNA, 3'
 end

Seq. No. 32748
 Contig ID 305661_1.R1040
 5'-most EST asn701141506.h1
 Method BLASTX
 NCBI GI g4416307
 BLAST score 308
 E value 4.0e-28
 Match length 104
 % identity 53
 NCBI Description (AF105716) hypothetical protein [Zea mays]

Seq. No. 32749
 Contig ID 305791_1.R1040
 5'-most EST g4397239
 Method BLASTN
 NCBI GI g169348
 BLAST score 50
 E value 4.0e-19
 Match length 212
 % identity 86
 NCBI Description P.vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3'
 end

Seq. No. 32750
 Contig ID 305867_1.R1040
 5'-most EST asn701141850.h1

Seq. No. 32751
 Contig ID 305957_1.R1040
 5'-most EST g4396382

Seq. No. 32752

% identity	60
NCBI Description	(AC000104) EST gb ATTS0956 comes from this gene. [Arabidopsis thaliana]
Seq. No.	32765
Contig ID	306850_1.R1040
5'-most EST	jC-gmf102220050b07a1
Seq. No.	32766
Contig ID	306873_1.R1040
5'-most EST	jC-gmle01810092g03d1
Method	BLASTX
NCBI GI	g3152583
BLAST score	229
E value	6.0e-19
Match length	90
% identity	54
NCBI Description	(AC002986) Contains similarity to inhibitor of apoptosis protein gb_U45881 from D. melanogaster. [Arabidopsis thaliana]
Seq. No.	32767
Contig ID	306888_1.R1040
5'-most EST	jC-gmle01810050c02d1
Method	BLASTN
NCBI GI	g2351071
BLAST score	40
E value	5.0e-13
Match length	116
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3, complete sequence [Arabidopsis thaliana]
Seq. No.	32768
Contig ID	306910_1.R1040
5'-most EST	jC-gmf102220050e04d1
Seq. No.	32769
Contig ID	306923_1.R1040
5'-most EST	jC-gmle01810036e03d1
Seq. No.	32770
Contig ID	306925_1.R1040
5'-most EST	jC-gmst02400065e10d1
Seq. No.	32771
Contig ID	306932_1.R1040
5'-most EST	jC-gmf102220050f05d1
Seq. No.	32772
Contig ID	306944_1.R1040
5'-most EST	jC-gmf102220050f11d1
Method	BLASTN
NCBI GI	g2924257
BLAST score	379
E value	0.0e+00
Match length	483

% identity 47
NCBI Description Tobacco chloroplast genome DNA

Seq. No. 32773
Contig ID 306951_1.R1040
5'-most EST jC-gmle01810050f02d1

Seq. No. 32774
Contig ID 306972_1.R1040
5'-most EST jC-gmle02220050h03a1
Method BLASTX
NCBI GI g3668077
BLAST score 125
E value 3.0e-09
Match length 67
% identity 55
NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32775
Contig ID 306975_1.R1040
5'-most EST jC-gmle01810050h04d1
Method BLASTX
NCBI GI g2447013
BLAST score 167
E value 1.0e-11
Match length 63
% identity 52
NCBI Description (D37949) defective F1F0-ATPase alpha subunit precursor [Saccharomyces cerevisiae]

Seq. No. 32776
Contig ID 307016_1.R1040
5'-most EST jC-gmle01810051b05d1
Method BLASTX
NCBI GI g3033392
BLAST score 283
E value 3.0e-25
Match length 85
% identity 65
NCBI Description (AC004238) putative translation initiation factor EIF-2B-epsilon subunit [Arabidopsis thaliana]

Seq. No. 32777
Contig ID 307024_1.R1040
5'-most EST jC-gmle02220051b10d1
Method BLASTN
NCBI GI g3319365
BLAST score 77
E value 5.0e-35
Match length 193
% identity 88
NCBI Description Arabidopsis thaliana BAC T24M8

Seq. No. 32778
Contig ID 307035_1.R1040
5'-most EST jC-gmle01810051c06d1

Seq. No. 32779
 Contig ID 307047_1.R1040
 5'-most EST jC-gmf102220051d01d1
 Method BLASTX
 NCBI GI g3047125
 BLAST score 174
 E value 2.0e-12
 Match length 38
 % identity 76
 NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 32780
 Contig ID 307063_1.R1040
 5'-most EST jC-gmle01810051e12d1

Seq. No. 32781
 Contig ID 307078_1.R1040
 5'-most EST jC-gmle01810067b08d1

Seq. No. 32782
 Contig ID 307091_1.R1040
 5'-most EST jC-gmf102220051f04d1
 Method BLASTX
 NCBI GI g4512682
 BLAST score 306
 E value 6.0e-28
 Match length 71
 % identity 82
 NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]

Seq. No. 32783
 Contig ID 307097_1.R1040
 5'-most EST jC-gmle01810051f07d1

Seq. No. 32784
 Contig ID 307115_1.R1040
 5'-most EST jC-gmle01810051g07d1

Seq. No. 32785
 Contig ID 307126_1.R1040
 5'-most EST uC-gmf1minsoy014e07b1
 Method BLASTX
 NCBI GI g2244816
 BLAST score 753
 E value 6.0e-80
 Match length 248
 % identity 27
 NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32786
 Contig ID 307129_1.R1040
 5'-most EST jC-gmf102220051h03a1
 Method BLASTX
 NCBI GI g1652745
 BLAST score 184
 E value 3.0e-13
 Match length 156

5'-most EST	jC-gmle01810053b07d1
Seq. No.	32808
Contig ID	307419_1.R1040
5'-most EST	jC-gmfl02220053h04d1
Seq. No.	32809
Contig ID	307422_1.R1040
5'-most EST	uC-gmflminsoy002d08b1
Seq. No.	32810
Contig ID	307434_1.R1040
5'-most EST	uC-gmrominsoyl00b10b1
Method	BLASTX
NCBI GI	g4262239
BLAST score	444
E value	7.0e-44
Match length	145
% identity	63
NCBI Description	(AC006200) putative membrane transporter [Arabidopsis thaliana]
Seq. No.	32811
Contig ID	307434_2.R1040
5'-most EST	jC-gmle01810002f05d1
Seq. No.	32812
Contig ID	307453_1.R1040
5'-most EST	jC-gmfl02220054b03d1
Seq. No.	32813
Contig ID	307485_1.R1040
5'-most EST	jC-gmfl02220054d04a1
Seq. No.	32814
Contig ID	307521_1.R1040
5'-most EST	jC-gmfl02220054f03d1
Seq. No.	32815
Contig ID	307527_1.R1040
5'-most EST	jC-gmle01810047g12d1
Seq. No.	32816
Contig ID	307529_1.R1040
5'-most EST	jC-gmle01810080h02d1
Seq. No.	32817
Contig ID	307561_1.R1040
5'-most EST	jC-gmle01810054h07d1
Seq. No.	32818
Contig ID	307611_1.R1040
5'-most EST	jC-gmle01810055c11a1
Seq. No.	32819
Contig ID	307641_1.R1040
5'-most EST	jC-gmfl02220055e11d1

Seq. No. 32832
 Contig ID 307882_1.R1040
 5'-most EST jC-gmro02910033f12d1

Seq. No. 32833
 Contig ID 307890_1.R1040
 5'-most EST uC-gmflminsoy055h09b1
 Method BLASTX
 NCBI GI g2648588
 BLAST score 294
 E value 2.0e-26
 Match length 156
 % identity 41
 NCBI Description (AE000968) Glu-tRNA amidotransferase, subunit A (gatA-1)
 [Archaeoglobus fulgidus]

Seq. No. 32834
 Contig ID 307909_1.R1040
 5'-most EST jC-gmle01810057f06d1

Seq. No. 32835
 Contig ID 307936_1.R1040
 5'-most EST jC-gmfl02220057h06d1

Seq. No. 32836
 Contig ID 307971_1.R1040
 5'-most EST jC-gmro02910036f01d1

Seq. No. 32837
 Contig ID 307995_1.R1040
 5'-most EST jC-gmfl02220058g10a1

Seq. No. 32838
 Contig ID 307997_1.R1040
 5'-most EST jC-gmst02400046h02d1

Seq. No. 32839
 Contig ID 307997_2.R1040
 5'-most EST jC-gmfl02220101g05d1

Seq. No. 32840
 Contig ID 308004_1.R1040
 5'-most EST jC-gmfl02220059b01d1

Seq. No. 32841
 Contig ID 308017_1.R1040
 5'-most EST uC-gmrominsoy212a10b1
 Method BLASTX
 NCBI GI g2894560
 BLAST score 563
 E value 7.0e-58
 Match length 187
 % identity 65
 NCBI Description (AL021890) putative protein [Arabidopsis thaliana]

Seq. No. 32842
 Contig ID 308039_1.R1040

5'-most EST jC-gmro02910075a06d1
 Method BLASTN
 NCBI GI g168214
 BLAST score 107
 E value 8.0e-53
 Match length 290
 % identity 85
 NCBI Description Hevea brasiliensis 3-hydroxy-3-methylglutaryl-coenzyme A reductase (hmgr3) mRNA, complete cds

Seq. No. 32915
 Contig ID 309786_1.R1040
 5'-most EST jC-gmfl02220077d05a1
 Method BLASTX
 NCBI GI g4314356
 BLAST score 299
 E value 7.0e-27
 Match length 144
 % identity 43
 NCBI Description (AC006340) putative anthocyanidin-3-glucoside rhamnosyltransferase [Arabidopsis thaliana]

Seq. No. 32916
 Contig ID 309805_1.R1040
 5'-most EST jC-gmfl02220077f05a1

Seq. No. 32917
 Contig ID 309806_1.R1040
 5'-most EST jC-gmfl02220077e06d1

Seq. No. 32918
 Contig ID 309826_1.R1040
 5'-most EST jC-gmfl02220077f08d1

Seq. No. 32919
 Contig ID 309849_1.R1040
 5'-most EST jC-gmfl02220077h01a1

Seq. No. 32920
 Contig ID 309902_1.R1040
 5'-most EST uC-gmrominsoy260b11b1

Seq. No. 32921
 Contig ID 309959_1.R1040
 5'-most EST jC-gmfl02220079b01d1

Seq. No. 32922
 Contig ID 309969_1.R1040
 5'-most EST jC-gmfl02220080h02d1

Seq. No. 32923
 Contig ID 310019_1.R1040
 5'-most EST g5175497

Seq. No. 32924
 Contig ID 310076_1.R1040
 5'-most EST jC-gmst02400017f07d1

00684015-101000

Contig ID 310446_1.R1040
5'-most EST jC-gmfl02220094a12a1

Seq. No. 32936
Contig ID 310447_1.R1040
5'-most EST jC-gmfl02220083e02a1
Method BLASTX
NCBI GI g2702268
BLAST score 588
E value 6.0e-61
Match length 163
% identity 64
NCBI Description (AC003033) putative cellulase [Arabidopsis thaliana]

Seq. No. 32937
Contig ID 310451_1.R1040
5'-most EST jC-gmfl02220083h10a1

Seq. No. 32938
Contig ID 310452_1.R1040
5'-most EST jC-gmfl02220083f08a1

Seq. No. 32939
Contig ID 310465_4.R1040
5'-most EST jC-gmfl02220099f03a1

Seq. No. 32940
Contig ID 310479_1.R1040
5'-most EST jC-gmfl02220083g08a1

Seq. No. 32941
Contig ID 310505_1.R1040
5'-most EST jC-gmfl02220083h12d1

Seq. No. 32942
Contig ID 310511_1.R1040
5'-most EST jC-gmfl02220101f11d1

Seq. No. 32943
Contig ID 310554_1.R1040
5'-most EST jC-gmfl02220084e02d1

Seq. No. 32944
Contig ID 310579_1.R1040
5'-most EST jC-gmfl02220084h09d1

Seq. No. 32945
Contig ID 310587_1.R1040
5'-most EST jC-gmfl02220112d07d1

Seq. No. 32946
Contig ID 310593_1.R1040
5'-most EST jC-gmst02400020h09a1
Method BLASTX
NCBI GI g3201611
BLAST score 270
E value 2.0e-23

Match length 44
 % identity 68
 NCBI Description (AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No. 32979
 Contig ID 311330_2.R1040
 5'-most EST jC-gmst02400008h07d1

Seq. No. 32980
 Contig ID 311347_1.R1040
 5'-most EST jC-gmfl02220092d03d1
 Method BLASTN
 NCBI GI g1044867
 BLAST score 43
 E value 8.0e-15
 Match length 47
 % identity 98
 NCBI Description Glycine max mRNA for cinnamic acid 4-hydroxylase (CYP73)

Seq. No. 32981
 Contig ID 311372_1.R1040
 5'-most EST jC-gmfl02220092f05d1
 Method BLASTX
 NCBI GI g4538965
 BLAST score 172
 E value 1.0e-12
 Match length 69
 % identity 54
 NCBI Description (AL049488) hypothetical protein [Arabidopsis thaliana]

Seq. No. 32982
 Contig ID 311377_1.R1040
 5'-most EST jC-gmfl02220092f12a1
 Method BLASTX
 NCBI GI g4530126
 BLAST score 604
 E value 1.0e-62
 Match length 210
 % identity 57
 NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No. 32983
 Contig ID 311380_1.R1040
 5'-most EST jC-gmfl02220092g02d1
 Method BLASTX
 NCBI GI g4101626
 BLAST score 402
 E value 8.0e-39
 Match length 89
 % identity 79
 NCBI Description (AF005096) desaturase/cytochrome b5 protein [Ricinus communis]

Seq. No. 32984
 Contig ID 311396_1.R1040

E value	2.0e-52
Match length	214
% identity	87
NCBI Description	V.faba VFCWINV1 mRNA for cell wall invertase I
Seq. No.	33029
Contig ID	312497_1.R1040
5'-most EST	jC-gmst02400053d10a1
Seq. No.	33030
Contig ID	312513_1.R1040
5'-most EST	jC-gmle01810061b01d1
Seq. No.	33031
Contig ID	312519_1.R1040
5'-most EST	jC-gmst02400056f08d1
Seq. No.	33032
Contig ID	312549_1.R1040
5'-most EST	jC-gmfl02220106b09a1
Method	BLASTX
NCBI GI	g4559356
BLAST score	218
E value	2.0e-17
Match length	183
% identity	8
NCBI Description	(AC006585) hypothetical protein [Arabidopsis thaliana]
Seq. No.	33033
Contig ID	312555_1.R1040
5'-most EST	jC-gmfl02220106c01a1
Seq. No.	33034
Contig ID	312673_1.R1040
5'-most EST	jC-gmfl02220108d10a1
Seq. No.	33035
Contig ID	312755_1.R1040
5'-most EST	jC-gmfl02220112d06d1
Seq. No.	33036
Contig ID	312763_1.R1040
5'-most EST	jC-gmfl02220112e07d1
Seq. No.	33037
Contig ID	312771_1.R1040
5'-most EST	g5057800
Method	BLASTX
NCBI GI	g2129929
BLAST score	376
E value	7.0e-36
Match length	174
% identity	44
NCBI Description	DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB2 - tomato >gi_1049068 (U28403) RNA polymerase II subunit 2 [Solanum lycopersicum]

[illegible]

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E value	4.0e-40
Match length	140
% identity	56
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]
Seq. No.	33062
Contig ID	313667_1.R1040
5'-most EST	uC-gmrominsoy0001h10a1
Seq. No.	33063
Contig ID	313704_1.R1040
5'-most EST	jC-gmfl02220132aa03d1
Seq. No.	33064
Contig ID	313778_1.R1040
5'-most EST	jC-gmfl02220132ae10a1
Method	BLASTN
NCBI GI	g167227
BLAST score	212
E value	1.0e-115
Match length	460
% identity	87
NCBI Description	Canavalia ensiformis urease (ure) mRNA, complete cds
Seq. No.	33065
Contig ID	313847_1.R1040
5'-most EST	jC-gmfl02220133f09a1
Seq. No.	33066
Contig ID	313851_1.R1040
5'-most EST	uC-gmropic104d10b1
Method	BLASTX
NCBI GI	g1773014
BLAST score	670
E value	2.0e-70
Match length	217
% identity	62
NCBI Description	(Y10338) chloride channel Stclcl [Solanum tuberosum]
Seq. No.	33067
Contig ID	313964_1.R1040
5'-most EST	jC-gmfl02220138a06d1
Seq. No.	33068
Contig ID	313966_1.R1040
5'-most EST	jC-gmro02910008h03a1
Method	BLASTX
NCBI GI	g4558550
BLAST score	659
E value	3.0e-69
Match length	156
% identity	79
NCBI Description	(AC007138) putative protein transport factor [Arabidopsis thaliana]
Seq. No.	33069

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Contig ID	314024_1.R1040
5'-most EST	jC-gmle01810048c01d1
Seq. No.	33070
Contig ID	314102_1.R1040
5'-most EST	jC-gmfl02220139d01d1
Seq. No.	33071
Contig ID	314128_1.R1040
5'-most EST	jC-gmfl02220139g07a1
Seq. No.	33072
Contig ID	314143_1.R1040
5'-most EST	jC-gmfl02220139h05d1
Seq. No.	33073
Contig ID	314172_1.R1040
5'-most EST	jC-gmfl02220140c03d1
Seq. No.	33074
Contig ID	314180_1.R1040
5'-most EST	g5510346
Method	BLASTX
NCBI GI	g509810
BLAST score	145
E value	5.0e-09
Match length	38
% identity	71
NCBI Description	(L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]
Seq. No.	33075
Contig ID	314242_1.R1040
5'-most EST	jC-gmfl02220141d01d1
Method	BLASTN
NCBI GI	g2104674
BLAST score	38
E value	5.0e-12
Match length	134
% identity	86
NCBI Description	V.faba mRNA for transcription factor containing bZIP
Seq. No.	33076
Contig ID	314259_1.R1040
5'-most EST	jC-gmfl02220141d11d1
Seq. No.	33077
Contig ID	314362_1.R1040
5'-most EST	jC-gmfl02220142d05d1
Seq. No.	33078
Contig ID	314363_1.R1040
5'-most EST	jC-gmfl02220142c06a1
Method	BLASTN
NCBI GI	g3641869
BLAST score	133
E value	1.0e-68
Match length	277

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

[illegible]

```
Method          BLASTN
NCBI GI         g310560
BLAST score     57
E value         6.0e-23
Match length    57
% identity      100
```

```
Method BLASTX
NCBI GI g133872
BLAST score 180
E value 4.0e-13
Match length 125
% identity 31
```

```
Method             BLASTX
NCBI GI            g1477565
BLAST score        191
E value            2.0e-14
Match length       143
% identity         7
```

```
Method          BLASTN
NCBI GI         g402243
BLAST score     184
E value         7.0e-99
Match length    455
% identity      85
```


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Method	BLASTX
NCBI GI	g1813489
BLAST score	154
E value	4.0e-10
Match length	70
% identity	50
NCBI Description	(U64312) amidase [Bacillus firmus]
Seq. No.	33107
Contig ID	315060_1.R1040
5'-most EST	jC-gmle01810001c11d1
Seq. No.	33108
Contig ID	315071_1.R1040
5'-most EST	jC-gmle01810001d10a1
Seq. No.	33109
Contig ID	315072_1.R1040
5'-most EST	jC-gmle01810048c11a1
Seq. No.	33110
Contig ID	315081_1.R1040
5'-most EST	jC-gmle01810001e09d1
Seq. No.	33111
Contig ID	315083_1.R1040
5'-most EST	jC-gmst02400004c11d1
Seq. No.	33112
Contig ID	315086_1.R1040
5'-most EST	jC-gmle01810017c11a2
Method	BLASTX
NCBI GI	g4006910
BLAST score	196
E value	6.0e-15
Match length	72
% identity	54
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]
Seq. No.	33113
Contig ID	315087_1.R1040
5'-most EST	jC-gmle01810001f03a1
Seq. No.	33114
Contig ID	315098_1.R1040
5'-most EST	jC-gmle01810001g01a1
Seq. No.	33115
Contig ID	315099_1.R1040
5'-most EST	jC-gmle01810001h01a1
Seq. No.	33116
Contig ID	315123_1.R1040
5'-most EST	jC-gmle01810001h10d1
Seq. No.	33117
Contig ID	315174_1.R1040

Seq. No. 33126
 Contig ID 315297_1.R1040
 5'-most EST jC-gmle01810003h03a1
 Method BLASTX
 NCBI GI g3063473
 BLAST score 345
 E value 2.0e-32
 Match length 97
 % identity 72
 NCBI Description (AC003981) F22013.35 [Arabidopsis thaliana]

Seq. No. 33127
 Contig ID 315313_1.R1040
 5'-most EST jC-gmle01810004a08d1
 Method BLASTX
 NCBI GI g1352934
 BLAST score 194
 E value 8.0e-15
 Match length 61
 % identity 59
 NCBI Description HYPOTHETICAL 161.2 KD PROTEIN IN NMD5-HOM6 INTERGENIC
 REGION >gi_1078403_pir_S57160 sulfite reductase homolog
 YJR137c - yeast (Saccharomyces cerevisiae)
 >gi_1015876_emb_CAA89669 (Z49637) ORF YJR137c
 [Saccharomyces cerevisiae]

Seq. No. 33128
 Contig ID 315315_1.R1040
 5'-most EST jC-gmle01810004a10a1
 Method BLASTX
 NCBI GI g3426037
 BLAST score 256
 E value 3.0e-37
 Match length 169
 % identity 35
 NCBI Description (AC005168) putative ABC transporter protein [Arabidopsis
 thaliana]

Seq. No. 33129
 Contig ID 315317_1.R1040
 5'-most EST jC-gmle01810004a11d1
 Method BLASTX
 NCBI GI g1931652
 BLAST score 677
 E value 4.0e-71
 Match length 226
 % identity 63
 NCBI Description (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog
 [Arabidopsis thaliana]

Seq. No. 33130
 Contig ID 315354_1.R1040
 5'-most EST jC-gmle01810004c09d1

Seq. No. 33131
 Contig ID 315383_1.R1040
 5'-most EST jC-gmle01810094b07d1

E value 2.0e-27
 Match length 153
 % identity 42
 NCBI Description URICASE (URATE OXIDASE) >gi_2131155_pir_JC5140 urate
 oxidase (EC 1.7.3.3) - yeast (Pichia jadinii)
 >gi_1741860_dbj_BAA06804_ (D32043) uricase [Candida utilis]

Seq. No. 33193
 Contig ID 317512_1.R1040
 5'-most EST jC-gmle01810023d07a1

Seq. No. 33194
 Contig ID 317513_1.R1040
 5'-most EST jC-gmle01810023d07d1

Seq. No. 33195
 Contig ID 317531_1.R1040
 5'-most EST jC-gmle01810023e06a1

Seq. No. 33196
 Contig ID 317597_1.R1040
 5'-most EST jC-gmle01810093b04a1

Seq. No. 33197
 Contig ID 317651_1.R1040
 5'-most EST jC-gmle01810024f10a1

Seq. No. 33198
 Contig ID 317682_1.R1040
 5'-most EST jC-gmst02400068d08d1
 Method BLASTX
 NCBI GI g2262113
 BLAST score 237
 E value 8.0e-20
 Match length 56
 % identity 73
 NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 33199
 Contig ID 317728_1.R1040
 5'-most EST jC-gmle01810025c04a1
 Method BLASTN
 NCBI GI g170073
 BLAST score 76
 E value 1.0e-34
 Match length 118
 % identity 92
 NCBI Description Soybean calmodulin (SCaM-3) mRNA, complete cds

Seq. No. 33200
 Contig ID 317748_1.R1040
 5'-most EST jC-gmro02910007d04d1

Seq. No. 33201
 Contig ID 317804_1.R1040
 5'-most EST jC-gmle01810025g10d1

Contig ID 317982_1.R1040
5'-most EST jC-gmst02400002e02d1

Seq. No. 33211
Contig ID 317997_1.R1040
5'-most EST jC-gmle01810035f12d1

Seq. No. 33212
Contig ID 318029_1.R1040
5'-most EST jC-gmle01810027f09d1

Seq. No. 33213
Contig ID 318075_1.R1040
5'-most EST jC-gmle01810028b02a1

Seq. No. 33214
Contig ID 318100_1.R1040
5'-most EST jC-gmst02400076d09a1
Method BLASTX
NCBI GI g2444174
BLAST score 604
E value 3.0e-78
Match length 176
% identity 79
NCBI Description (U94781) unconventional myosin [Helianthus annuus]

Seq. No. 33215
Contig ID 318109_1.R1040
5'-most EST jC-gmro02910061e02d1
Method BLASTX
NCBI GI g2832241
BLAST score 186
E value 1.0e-13
Match length 87
% identity 28
NCBI Description (AF030864) nonphototropic hypocotyl 1 [Arabidopsis thaliana]

Seq. No. 33216
Contig ID 318121_1.R1040
5'-most EST jC-gmle01810064b01a1

Seq. No. 33217
Contig ID 318132_1.R1040
5'-most EST jC-gmle01810035f08d1

Seq. No. 33218
Contig ID 318144_1.R1040
5'-most EST jC-gmle01810028f05d1

Seq. No. 33219
Contig ID 318146_1.R1040
5'-most EST uC-gmropic0001g04a1
Method BLASTX
NCBI GI g2088651
BLAST score 201
E value 3.0e-15

5'-most EST jC-gmle01810030d11a2
 Method BLASTX
 NCBI GI g3413511
 BLAST score 441
 E value 1.0e-43
 Match length 129
 % identity 66
 NCBI Description (AJ000265) glucose-6-phosphate isomerase [Spinacia oleracea]

Seq. No. 33230
 Contig ID 318377_1.R1040
 5'-most EST jC-gmle01810030d11d1
 Method BLASTX
 NCBI GI g4220528
 BLAST score 506
 E value 2.0e-51
 Match length 106
 % identity 89
 NCBI Description (AL035356) glucose-6-phosphate isomerase [Arabidopsis thaliana]

Seq. No. 33231
 Contig ID 318388_1.R1040
 5'-most EST jC-gmle01810078h03d1

Seq. No. 33232
 Contig ID 318452_1.R1040
 5'-most EST jC-gmle01810031a05a2
 Method BLASTX
 NCBI GI g2262157
 BLAST score 311
 E value 2.0e-44
 Match length 173
 % identity 60
 NCBI Description (AC002329) putative ligand-gated ion channel protein [Arabidopsis thaliana]

Seq. No. 33233
 Contig ID 318458_1.R1040
 5'-most EST jC-gmle01810033e03d1

Seq. No. 33234
 Contig ID 318459_1.R1040
 5'-most EST jC-gmle01810033e05d1

Seq. No. 33235
 Contig ID 318490_1.R1040
 5'-most EST jC-gmle01810033g05d1

Seq. No. 33236
 Contig ID 318511_1.R1040
 5'-most EST jC-gmst02400016c09d1
 Method BLASTX
 NCBI GI g4262162
 BLAST score 277
 E value 2.0e-24

Seq. No.	33246
Contig ID	318654_1.R1040
5'-most EST	jC-qmle01810094f09d1

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Seq. No.          33247
Contig ID         318680_1.R1040
5'-most EST      jC-qmle01810033b01a2
```

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Seq. No.          33248
Contig ID         318697_1.R1040
5'-most EST      jC-gmle01810033c01d1
```

```
Seq. No.          33249
Contig ID         318742_1.R1040
5'-most EST      jC-qmle01810033e08a2
```

```
Seq. No.          33250
Contig ID         318748_1.R1040
5'-most EST      jC-qmle01810033e12d1
```

```
Seq. No.          33251
Contig ID         318801_1.R1040
5'-most EST      jC-qmle01810034a06d1
```

```
Seq. No.          33252
Contig ID         318809_1.R1040
5'-most EST      iC-qmle01810034a11d1
```

```
Seq. No.          33253
Contig ID         318848_1.R1040
5'-most EST      jC-gmle01810034e02d1
Method            BLASTX
NCBI GI           g4559327
BLAST score       257
E value           4.0e-22
Match length      122
% identity        48
NCBI Description  (AC007087) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.          33254
Contig ID         318891_1.R1040
5'-most EST      iC-qmle01810034h09d1
```

```
Seq. No.          33255
Contig ID         318919_1.R1040
5'-most EST      iC-qmle01810035b04a2
```

```
Seq. No.          33256
Contig ID         318923_1.R1040
5'-most EST      jC-gmro02910075g03d1
Method            BLASTX
NCBI GI           g3935170
BLAST score       239
E value           4.0e-20
Match length      59
% identity        76
NCBI Description  (AC004557) F17L21.13 [Arabidopsis thaliana]
```


Contig ID	319211_1.R1040
5'-most EST	jC-gmro02910013f08d1
Seq. No.	33264
Contig ID	319222_1.R1040
5'-most EST	jC-gmle01810038b04d1
Seq. No.	33265
Contig ID	319231_1.R1040
5'-most EST	jC-gmle01810038d07d1
Seq. No.	33266
Contig ID	319294_1.R1040
5'-most EST	jC-gmle01810040d07a1
Seq. No.	33267
Contig ID	319352_1.R1040
5'-most EST	jC-gmle01810040h10d1
Method	BLASTN
NCBI GI	g3335331
BLAST score	36
E value	1.0e-10
Match length	56
% identity	91
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	33268
Contig ID	319356_1.R1040
5'-most EST	jC-gmle01810041a02a1
Method	BLASTX
NCBI GI	g2829870
BLAST score	249
E value	3.0e-21
Match length	89
% identity	25
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	33269
Contig ID	319360_1.R1040
5'-most EST	jC-gmle01810041a06a1
Seq. No.	33270
Contig ID	319429_1.R1040
5'-most EST	jC-gmle01810041f11a1
Method	BLASTX
NCBI GI	g2077896
BLAST score	393
E value	5.0e-38
Match length	153
% identity	49
NCBI Description	(AB003470) beta-D-glucosidase [Aspergillus kawachii]
Seq. No.	33271
Contig ID	319467_1.R1040
5'-most EST	jC-gmle01810042d10a1

Seq. No.	33272
Contig ID	319482_1.R1040
5'-most EST	jC-qmle01810042b06a1

```
Seq. No.          33273
Contig ID         319692_1.R1040
5'-most EST      jC-qmle01810044c09a1
```

```
Seq. No.      33274
Contig ID     319703_1.R1040
5'-most EST   jC-qmle01810043e05d1
```

```
Seq. No.          33275
Contig ID         319706_1.R1040
5'-most EST      jC-qmle01810043e07d1
```

Seq. No.	33276
Contig ID	319738_1.R1040
5'-most EST	jC-qmle01810043q03d1

```
Seq. No.          33277
Contig ID         319770_1.R1040
5'-most EST      jC-gmst02400073e09d1
```

```
Seq. No.          33278
Contig ID         319818_1.R1040
5'-most EST      jC-qmle01810044b11d1
```

```
Seq. No.          33279
Contig ID         319840_1.R1040
5'-most EST      jC-gmle01810044c11a1
Method            BLASTX
NCBI GI           g3560136
BLAST score       505
E value           3.0e-51
Match length      166
% identity        55
```

NCBI Description (AL031534) 2-isopropylmalate synthase. [Schizosaccharomyces pombe]

Seq. No.	33280
Contig ID	319841_1.R1040
5'-most EST	jC-qmle01810044c11d1

```
Seq. No.          33281
Contig ID         320112_1.R1040
5'-most EST      jC-gmle01810046e06a1
```

```
Seq. No.          33282
Contig ID         320136_1.R1040
5'-most EST      jC-gml_e01810046d05a1
Method            BLASTX
NCBI GI           g3688186
BLAST score       557
E value           2.0e-57
Match length      139
% identity        73
```


NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 33283
Contig ID 320192_1.R1040
5'-most EST jC-gmle01810046f05d1
Method BLASTX
NCBI GI g4314371
BLAST score 148
E value 1.0e-09
Match length 40
% identity 65

NCBI Description (AC006340) putative G9a protein [Arabidopsis thaliana]

Seq. No. 33284
Contig ID 320313_1.R1040
5'-most EST uC-gmropic014b11b1

Seq. No. 33285
Contig ID 320315_1.R1040
5'-most EST jC-gmst02400020da07d1

Seq. No. 33286
Contig ID 320407_1.R1040
5'-most EST jC-gmle01810048b12d1

Seq. No. 33287
Contig ID 320438_1.R1040
5'-most EST jC-gmle01810048d09d1

Seq. No. 33288
Contig ID 320446_1.R1040
5'-most EST jC-gmle01810048e03a1

Seq. No. 33289
Contig ID 320447_1.R1040
5'-most EST jC-gmle01810048e03d1

Seq. No. 33290
Contig ID 320552_1.R1040
5'-most EST jC-gmle01810049d06d1

Seq. No. 33291
Contig ID 320558_1.R1040
5'-most EST jC-gmle01810049e01d1

Seq. No. 33292
Contig ID 320642_1.R1040
5'-most EST jC-gmle01810050e10a1
Method BLASTN
NCBI GI g11576
BLAST score 433
E value 0.0e+00
Match length 465
% identity 98

NCBI Description Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val, NADH dehydrogenase and ORF

5'-most EST jC-gmle01810065d12d1

 Seq. No. 33329
 Contig ID 322297_1.R1040
 5'-most EST jC-gmle01810065f08d1
 Method BLASTX
 NCBI GI g1408460
 BLAST score 252
 E value 1.0e-21
 Match length 124
 % identity 44
 NCBI Description (U40161) type 2A protein serine/threonine phosphatase 55
 kDa B regulatory subunit [Arabidopsis thaliana]

Seq. No. 33330
 Contig ID 322310_1.R1040
 5'-most EST jC-gmle01810065g11d1
 Method BLASTN
 NCBI GI g2764523
 BLAST score 114
 E value 3.0e-57
 Match length 342
 % identity 83
 NCBI Description Pisum sativum mRNA for Rieske iron-sulfur protein Tic55

Seq. No. 33331
 Contig ID 322322_1.R1040
 5'-most EST jC-gmst02400044g03d1

Seq. No. 33332
 Contig ID 322344_1.R1040
 5'-most EST jC-gmle01810066c12d1

Seq. No. 33333
 Contig ID 322347_1.R1040
 5'-most EST jC-gmle01810066d03d1

Seq. No. 33334
 Contig ID 322365_1.R1040
 5'-most EST jC-gmro02910019a06d1

Seq. No. 33335
 Contig ID 322382_1.R1040
 5'-most EST jC-gmst02400032h02a1
 Method BLASTX
 NCBI GI g1350528
 BLAST score 147
 E value 3.0e-09
 Match length 39
 % identity 64
 NCBI Description (L47602) ABA-responsive and embryogenesis-associated gene;
 LEA-like protein [Picea glauca]

Seq. No. 33336
 Contig ID 322391_1.R1040
 5'-most EST jC-gmle01810067a02d1

Seq. No. 33337
 Contig ID 322395_1.R1040
 5'-most EST jC-gmst02400074f02d1

Seq. No. 33338
 Contig ID 322406_1.R1040
 5'-most EST jC-gmle01810073a03d1

Seq. No. 33339
 Contig ID 322474_1.R1040
 5'-most EST jC-gmle01810067g03a1

Seq. No. 33340
 Contig ID 322488_1.R1040
 5'-most EST jC-gmle01810067h01d1

Seq. No. 33341
 Contig ID 322501_1.R1040
 5'-most EST jC-gmst02400027a09d1

Seq. No. 33342
 Contig ID 322524_1.R1040
 5'-most EST jC-gmle01810068b08a1

Seq. No. 33343
 Contig ID 322532_1.R1040
 5'-most EST jC-gmle01810068c02a1
 Method BLASTX
 NCBI GI g1710055
 BLAST score 328
 E value 2.0e-30
 Match length 118
 % identity 54
 NCBI Description RDS1 PROTEIN >gi_1363621_pir_S58477 rds1 protein - fission yeast (Schizosaccharomyces pombe) >gi_1184029_emb_CAA54544_(X77328) rds1 [Schizosaccharomyces pombe]

Seq. No. 33344
 Contig ID 322554_1.R1040
 5'-most EST jC-gmle01810071d01a1

Seq. No. 33345
 Contig ID 322578_1.R1040
 5'-most EST jC-gmle01810068e10d1

Seq. No. 33346
 Contig ID 322583_1.R1040
 5'-most EST jC-gmle01810068f02d1

Seq. No. 33347
 Contig ID 322609_1.R1040
 5'-most EST jC-gmle01810068g10d1

Seq. No. 33348
 Contig ID 322615_1.R1040
 5'-most EST jC-gmle01810068h05a1

09684016-101000

Seq. No. 33349
Contig ID 322618_1.R1040
5'-most EST jC-gmle01810068h08a1

Seq. No. 33350
Contig ID 322650_1.R1040
5'-most EST jC-gmle01810069e03d1

Seq. No. 33351
Contig ID 322682_1.R1040
5'-most EST jC-gmle01810070a11a1

Seq. No. 33352
Contig ID 322705_1.R1040
5'-most EST jC-gmle01810070c04d1
Method BLASTX
NCBI GI g3924606
BLAST score 324
E value 1.0e-30
Match length 89
% identity 75
NCBI Description (AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No. 33353
Contig ID 322740_1.R1040
5'-most EST jC-gmle01810070e12a1
Method BLASTX
NCBI GI g2827534
BLAST score 685
E value 2.0e-72
Match length 150
% identity 86
NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 33354
Contig ID 322741_1.R1040
5'-most EST jC-gmle01810070f11d1

Seq. No. 33355
Contig ID 322763_1.R1040
5'-most EST jC-gmle01810070g02d1

Seq. No. 33356
Contig ID 322775_1.R1040
5'-most EST jC-gmle01810070h09a1

Seq. No. 33357
Contig ID 322776_1.R1040
5'-most EST jC-gmle01810070h09d1

Seq. No. 33358
Contig ID 322850_1.R1040
5'-most EST jC-gmle01810071d12a1

Seq. No. 33359
Contig ID 322857_1.R1040
5'-most EST jC-gmle01810071e05d1

Seq. No. 33360
 Contig ID 322864_1.R1040
 5'-most EST fC-gmro700565119r2

Seq. No. 33361
 Contig ID 322871_1.R1040
 5'-most EST jC-gmle01810071f03d1
 Method BLASTX
 NCBI GI g3881976
 BLAST score 497
 E value 2.0e-50
 Match length 118
 % identity 76
 NCBI Description (AJ012409) hypothetical protein [Homo sapiens]

Seq. No. 33362
 Contig ID 322878_1.R1040
 5'-most EST jC-gmle01810071f08d1

Seq. No. 33363
 Contig ID 322886_1.R1040
 5'-most EST jC-gmle01810071g02d1

Seq. No. 33364
 Contig ID 322908_1.R1040
 5'-most EST jC-gmle01810071h06d1

Seq. No. 33365
 Contig ID 322922_1.R1040
 5'-most EST jC-gmle01810072b04d1

Seq. No. 33366
 Contig ID 322953_1.R1040
 5'-most EST jC-gmle01810072d06d1
 Method BLASTX
 NCBI GI g1710055
 BLAST score 188
 E value 4.0e-14
 Match length 100
 % identity 39
 NCBI Description RDS1 PROTEIN >gi_1363621_pir_S58477 rds1 protein - fission yeast (Schizosaccharomyces pombe) >gi_1184029_emb_CAA54544_(X77328) rds1 [Schizosaccharomyces pombe]

Seq. No. 33367
 Contig ID 322972_1.R1040
 5'-most EST jC-gmst02400006b09d1
 Method BLASTX
 NCBI GI g2739309
 BLAST score 394
 E value 4.0e-38
 Match length 91
 % identity 47
 NCBI Description (Y15990) P-glycoprotein-like protein [Arabidopsis thaliana]

Seq. No. 33368

NCBI Description 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE PRECURSOR
(3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)
>gi_1084385_pir_S22450 3-oxoacyl-[acyl-carrier-protein]
reductase (EC 1.1.1.100) precursor - Cuphea lanceolata
>gi_18046_emb_CAA45866 (X64566) 3-oxoacyl-[acyl-carrier
protein] reductase [Cuphea lanceolata]
>gi_228929_prf_1814446A beta ketoacyl-ACP reductase
[Cuphea lanceolata]

Seq. No. 33383
Contig ID 323601_1.R1040
5'-most EST jC-gmle01810082a09a1

Seq. No. 33384
Contig ID 323697_1.R1040
5'-most EST jC-gmle01810082f10a1
Method BLASTX
NCBI GI g479413
BLAST score 987
E value 1.0e-107
Match length 216
% identity 91
NCBI Description myosin-like protein - Arabidopsis thaliana

Seq. No. 33385
Contig ID 323815_1.R1040
5'-most EST jC-gmle01810083e02d1

Seq. No. 33386
Contig ID 323831_1.R1040
5'-most EST jC-gmle01810083e11a1

Seq. No. 33387
Contig ID 323850_1.R1040
5'-most EST jC-gmle01810083f10a1
Method BLASTX
NCBI GI g731810
BLAST score 404
E value 3.0e-39
Match length 109
% identity 67
NCBI Description PROBABLE 60S RIBOSOMAL PROTEIN YIL052C

>gi_626886_pir_S48427 ribosomal protein L34.e.B, cytosolic
- yeast (Saccharomyces cerevisiae) >gi_557816_emb_CAA86170_
(Z38060) spliced ribosomal protein, len: 121, CAI: 0.77,
RL34_RAT P11250 60S RIBOSOMAL PROTEIN L34 [Saccharomyces
cerevisiae]

Seq. No. 33388
Contig ID 323872_1.R1040
5'-most EST jC-gmle01810083g11a1
Method BLASTX
NCBI GI g4006908
BLAST score 217
E value 4.0e-17
Match length 78
% identity 53

Seq. No. 33398
 Contig ID 324231_1.R1040
 5'-most EST jC-gmle01810086e02a1

Seq. No. 33399
 Contig ID 324238_1.R1040
 5'-most EST jC-gmle01810086e06a1
 Method BLASTX
 NCBI GI g2765817
 BLAST score 382
 E value 1.0e-36
 Match length 175
 % identity 53
 NCBI Description (Z95352) AtMlo-h1 [Arabidopsis thaliana]
 >gi_3892049_gb_AAC78258.1_AAC78258 (AC002330) AtMlo-h1
 [Arabidopsis thaliana]

Seq. No. 33400
 Contig ID 324262_1.R1040
 5'-most EST jC-gmle01810086f07a1
 Method BLASTX
 NCBI GI g3913996
 BLAST score 305
 E value 3.0e-31
 Match length 109
 % identity 68
 NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR
 >gi_2208927_dbj_BAA20482_ (D85610) ATP-dependent protease
 Lon [Spinacia oleracea]

Seq. No. 33401
 Contig ID 324322_1.R1040
 5'-most EST jC-gmle01810087a08d1

Seq. No. 33402
 Contig ID 324382_1.R1040
 5'-most EST jC-gmle01810087d11a1

Seq. No. 33403
 Contig ID 324400_1.R1040
 5'-most EST jC-gmle01810087e09a1
 Method BLASTX
 NCBI GI g1172441
 BLAST score 167
 E value 3.0e-11
 Match length 53
 % identity 68
 NCBI Description POSSIBLE TRANSCRIPTION FACTOR POSF21 >gi_99685_pir_S21883
 DNA-binding protein POSF21 - Arabidopsis thaliana
 >gi_16429_emb_CAA43366_ (X61031) posF21 [Arabidopsis
 thaliana]

Seq. No. 33404
 Contig ID 324501_1.R1040
 5'-most EST jC-gmle01810088b11a1
 Method BLASTX
 NCBI GI g3176709

BLAST score 276
 E value 9.0e-27
 Match length 107
 % identity 52
 NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana]

Seq. No. 33413
 Contig ID 324878_1.R1040
 5'-most EST jC-gmle01810090e11a1
 Method BLASTX
 NCBI GI g4185136
 BLAST score 411
 E value 6.0e-40
 Match length 216
 % identity 40
 NCBI Description (AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No. 33414
 Contig ID 325006_1.R1040
 5'-most EST jC-gmle01810091c12d1

Seq. No. 33415
 Contig ID 325066_1.R1040
 5'-most EST uC-gmropic100f07b1
 Method BLASTX
 NCBI GI g2864618
 BLAST score 413
 E value 3.0e-40
 Match length 131
 % identity 57
 NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 33416
 Contig ID 325068_1.R1040
 5'-most EST jC-gmle01810091f10d1

Seq. No. 33417
 Contig ID 325075_1.R1040
 5'-most EST jC-gmle01810094h06d1

Seq. No. 33418
 Contig ID 325111_1.R1040
 5'-most EST jC-gmle01810092a04d1

Seq. No. 33419
 Contig ID 325157_1.R1040
 5'-most EST jC-gmle01810092d11a1

Seq. No. 33420
 Contig ID 325265_1.R1040
 5'-most EST jC-gmro02800032a06d1
 Method BLASTX
 NCBI GI g3924602
 BLAST score 152
 E value 8.0e-10
 Match length 51

% identity	51
NCBI Description	(AF069442) predicted OR23 protein of unknown function [Arabidopsis thaliana]
Seq. No.	33421
Contig ID	325314_1.R1040
5'-most EST	uC-gmflminsoy054h11b1
Method	BLASTX
NCBI GI	g4220477
BLAST score	284
E value	8.0e-38
Match length	133
% identity	68
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.	33422
Contig ID	325321_1.R1040
5'-most EST	jC-gmle01810093d12a1
Seq. No.	33423
Contig ID	325372_1.R1040
5'-most EST	jC-gmst02400036g05d2
Seq. No.	33424
Contig ID	325462_1.R1040
5'-most EST	jC-gmle01810094h07d1
Seq. No.	33425
Contig ID	325477_1.R1040
5'-most EST	jC-gmle01810094d12a1
Method	BLASTN
NCBI GI	g1839634
BLAST score	292
E value	1.0e-163
Match length	502
% identity	91
NCBI Description	heat shock protein 70=allergenic polypeptide (C-terminal, variable region) [Cladosporium herbarum, IMI 96220, mRNA Partial, 1061 nt]
Seq. No.	33426
Contig ID	325484_1.R1040
5'-most EST	jC-gmle01810094e04a1
Method	BLASTX
NCBI GI	g2980784
BLAST score	651
E value	3.0e-68
Match length	201
% identity	12
NCBI Description	(AL022198) puative protein [Arabidopsis thaliana]
Seq. No.	33427
Contig ID	325675_1.R1040
5'-most EST	jC-gmst02400064a11d1
Seq. No.	33428
Contig ID	325725_1.R1040

5'-most EST jC-gmro02800026c03a1
 Method BLASTX
 NCBI GI g2244866
 BLAST score 323
 E value 6.0e-30
 Match length 134
 % identity 58
 NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 33429
 Contig ID 325785_1.R1040
 5'-most EST jC-gmro02910071c01a1
 Method BLASTX
 NCBI GI g2459431
 BLAST score 298
 E value 7.0e-27
 Match length 91
 % identity 63
 NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]

Seq. No. 33430
 Contig ID 325792_1.R1040
 5'-most EST jC-gmro02800027d02d1

Seq. No. 33431
 Contig ID 325805_1.R1040
 5'-most EST jC-gmro02910022a11a1
 Method BLASTX
 NCBI GI g2832304
 BLAST score 210
 E value 2.0e-30
 Match length 149
 % identity 49
 NCBI Description (AF044489) receptor-like protein kinase [Oryza sativa]

Seq. No. 33432
 Contig ID 325884_1.R1040
 5'-most EST jC-gmro02800028e10a1
 Method BLASTX
 NCBI GI g3261631
 BLAST score 177
 E value 2.0e-12
 Match length 105
 % identity 42
 NCBI Description (Z79700) accA2 [Mycobacterium tuberculosis]

Seq. No. 33433
 Contig ID 325981_1.R1040
 5'-most EST jC-gmro02800029e04a1

Seq. No. 33434
 Contig ID 326038_1.R1040
 5'-most EST jC-gmro02800030a04d1
 Method BLASTX
 NCBI GI g2129623
 BLAST score 204
 E value 5.0e-16

Match length 73
 % identity 53
 NCBI Description immunophilin FKBP15-2 - Arabidopsis thaliana >gi_1272408
 (U52047) immunophilin [Arabidopsis thaliana]

Seq. No. 33435
 Contig ID 326093_1.R1040
 5'-most EST jC-gmro02800042c08d1
 Method BLASTX
 NCBI GI g3785990
 BLAST score 203
 E value 8.0e-16
 Match length 55
 % identity 73
 NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana]
 >gi_4220487 (AC006069) hypothetical protein [Arabidopsis
 thaliana]

Seq. No. 33436
 Contig ID 326100_1.R1040
 5'-most EST jC-gmro02800030e11d1

Seq. No. 33437
 Contig ID 326152_1.R1040
 5'-most EST jC-gmro02800031a04d1

Seq. No. 33438
 Contig ID 326177_1.R1040
 5'-most EST jC-gmro02800031b07a1
 Method BLASTX
 NCBI GI g1762584
 BLAST score 114
 E value 4.0e-09
 Match length 61
 % identity 49
 NCBI Description (U63373) polygalacturonase isoenzyme 1 beta subunit homolog
 [Arabidopsis thaliana]

Seq. No. 33439
 Contig ID 326216_1.R1040
 5'-most EST jC-gmro02800031d09d1

Seq. No. 33440
 Contig ID 326292_1.R1040
 5'-most EST g4301729

Seq. No. 33441
 Contig ID 326300_1.R1040
 5'-most EST jC-gmro02800032a05d1

Seq. No. 33442
 Contig ID 326318_1.R1040
 5'-most EST g4284526
 Method BLASTX
 NCBI GI g4335745
 BLAST score 362
 E value 2.0e-34

Match length 159
 % identity 47
 NCBI Description (AC006284) putative hydrolase (contains an
 esterase/lipase/thioesterase active site serine domain
 (prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 33443
 Contig ID 326500_1.R1040
 5'-most EST jC-gmro02800033d09d1

Seq. No. 33444
 Contig ID 326611_1.R1040
 5'-most EST jC-gmro02800034f06a1

Seq. No. 33445
 Contig ID 326612_1.R1040
 5'-most EST jC-gmro02800034f07a1
 Method BLASTX
 NCBI GI g1730576
 BLAST score 246
 E value 6.0e-21
 Match length 82
 % identity 56
 NCBI Description PROLINE IMINOPEPTIDASE (PROLYL AMINOPEPTIDASE)
 >gi_1084134_pir_JC4184 prolyl aminopeptidase (EC 3.4.11.5)
 - Aeromonas sobria >gi_1236731_dbj_BAA06380_ (D30714)
 prolyl aminopeptidase [Aeromonas sobria]

Seq. No. 33446
 Contig ID 326622_1.R1040
 5'-most EST jC-gmro02800035a04a1
 Method BLASTX
 NCBI GI g4510368
 BLAST score 170
 E value 5.0e-12
 Match length 106
 % identity 40
 NCBI Description (AC007017) putative transcription factor E2F5 [Arabidopsis
 thaliana]

Seq. No. 33447
 Contig ID 326711_1.R1040
 5'-most EST g4260415

Seq. No. 33448
 Contig ID 326733_1.R1040
 5'-most EST uC-gmrominsoy235e07b1
 Method BLASTX
 NCBI GI g2739381
 BLAST score 350
 E value 5.0e-33
 Match length 126
 % identity 60
 NCBI Description (AC002505) putative patatin [Arabidopsis thaliana]

Seq. No. 33449
 Contig ID 326800_1.R1040

09684016-1000

```
Seq. No.          33451
Contig ID         326831_1.R1040
5'-most EST      jC-gmr002800038f08d1
Method            BLASTN
NCBI GI           g1432053
BLAST score       62
E value           3.0e-26
Match length      170
% identity        84
NCBI Description  Oryza sativa asparagine synthetase mRNA, complete cds
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Seq. No.          33453
Contig ID         326950_1.R1040
5'-most EST      jC-gmr002910024g05d1
Method            BLASTX
NCBI GI           g2865394
BLAST score       141
E value           1.0e-08
Match length      49
% identity        57
NCBI Description  (AF036949) basic leucine zipper protein [Zea mays]
```

Seq. No.	33455
Contig ID	327251_1.R1040
5'-most EST	uC-gmrominsoy048h09b1

5'-most EST	jC-gmro02910002d04d1
Seq. No.	33465
Contig ID	327512_1.R1040
5'-most EST	jC-gmro02910002d11d1
Seq. No.	33466
Contig ID	327580_1.R1040
5'-most EST	jC-gmro02910002h12d1
Method	BLASTX
NCBI GI	g4235430
BLAST score	216
E value	2.0e-17
Match length	56
% identity	71
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]
Seq. No.	33467
Contig ID	327599_1.R1040
5'-most EST	jC-gmst02400069e02a1
Seq. No.	33468
Contig ID	327716_1.R1040
5'-most EST	jC-gmro02910004e12d1
Seq. No.	33469
Contig ID	327718_1.R1040
5'-most EST	jC-gmro02910016a08a1
Method	BLASTX
NCBI GI	g4510339
BLAST score	468
E value	7.0e-47
Match length	163
% identity	57
NCBI Description	(AC006921) putative ABC transporter protein [Arabidopsis thaliana]
Seq. No.	33470
Contig ID	327719_1.R1040
5'-most EST	jC-gmro02910004f03d1
Method	BLASTX
NCBI GI	g4510339
BLAST score	223
E value	3.0e-18
Match length	62
% identity	61
NCBI Description	(AC006921) putative ABC transporter protein [Arabidopsis thaliana]
Seq. No.	33471
Contig ID	327729_1.R1040
5'-most EST	uC-gmflminsoy065c02b1
Seq. No.	33472
Contig ID	327751_1.R1040
5'-most EST	jC-gmst02400051d03d1
Method	BLASTX

NCBI GI g3335169
 BLAST score 160
 E value 8.0e-11
 Match length 70
 % identity 47
 NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
 >gi_4455197_emb_CAB36520_(AL035440) embryo-specific
 protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No. 33473
 Contig ID 327939_1.R1040
 5'-most EST jC-gmro02910007f07a1
 Method BLASTX
 NCBI GI g2464865
 BLAST score 516
 E value 2.0e-52
 Match length 136
 % identity 69
 NCBI Description (Z99707) pectinesterase like protein [Arabidopsis thaliana]

Seq. No. 33474
 Contig ID 327940_1.R1040
 5'-most EST jC-gmro02910007f07d1
 Method BLASTX
 NCBI GI g3152618
 BLAST score 361
 E value 2.0e-34
 Match length 97
 % identity 67
 NCBI Description (AC004482) putative pectinesterase [Arabidopsis thaliana]
 >gi_3242724_(AC003040) putative pectinesterase [Arabidopsis
 thaliana]

Seq. No. 33475
 Contig ID 327993_1.R1040
 5'-most EST jC-gmro02910008h07a1

Seq. No. 33476
 Contig ID 327999_1.R1040
 5'-most EST jC-gmro02910006e11a1
 Method BLASTX
 NCBI GI g1669341
 BLAST score 182
 E value 2.0e-13
 Match length 57
 % identity 65
 NCBI Description (D45066) AOBP (ascorbate oxidase promoter-binding protein)
 [Cucurbita maxima]

Seq. No. 33477
 Contig ID 328018_1.R1040
 5'-most EST uC-gmropic070h10b1

Seq. No. 33478
 Contig ID 328023_1.R1040
 5'-most EST uC-gmronoir064f05b1

Seq. No. 33479
 Contig ID 328063_1.R1040
 5'-most EST uC-gmrnoir042e08b1
 Method BLASTX
 NCBI GI g4539343
 BLAST score 614
 E value 7.0e-64
 Match length 181
 % identity 70
 NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 33480
 Contig ID 328076_1.R1040
 5'-most EST jC-gmst02400027f03a1

Seq. No. 33481
 Contig ID 328194_1.R1040
 5'-most EST jC-gmro02910007h12a1

Seq. No. 33482
 Contig ID 328339_2.R1040
 5'-most EST jC-gmro02910008g10d1
 Method BLASTX
 NCBI GI g4107480
 BLAST score 155
 E value 3.0e-10
 Match length 59
 % identity 35
 NCBI Description (AL035085) putative mitochondrial carrier protein [Schizosaccharomyces pombe]

Seq. No. 33483
 Contig ID 328484_1.R1040
 5'-most EST uC-gmrnoir060d02b1
 Method BLASTX
 NCBI GI g2462833
 BLAST score 207
 E value 5.0e-16
 Match length 236
 % identity 24
 NCBI Description (AF000657) highly similar to froha and frohb, potential frohc [Arabidopsis thaliana]

Seq. No. 33484
 Contig ID 328495_1.R1040
 5'-most EST uC-gmropic044c09b1
 Method BLASTX
 NCBI GI g3367574
 BLAST score 181
 E value 3.0e-13
 Match length 109
 % identity 40
 NCBI Description (AL031135) hypothetical protein [Arabidopsis thaliana]

Seq. No. 33485
 Contig ID 328567_1.R1040
 5'-most EST jC-gmro02910040e08d1

BLAST score	248
E value	3.0e-21
Match length	135
% identity	49
NCBI Description	(AC003952) putative senescence-assoc. rhodanese-like protein [Arabidopsis thaliana]
Seq. No.	33494
Contig ID	328828_1.R1040
5'-most EST	jC-gmro02910013c04a1
Method	BLASTX
NCBI GI	g2245055
BLAST score	162
E value	6.0e-11
Match length	67
% identity	49
NCBI Description	(Z97342) resistance gene homolog (fragment) [Arabidopsis thaliana]
Seq. No.	33495
Contig ID	328849_1.R1040
5'-most EST	jC-gmst02400014c12d1
Method	BLASTX
NCBI GI	g2117619
BLAST score	189
E value	3.0e-14
Match length	72
% identity	50
NCBI Description	peroxidase (EC 1.11.1.7) 4 precursor - wheat >gi_732976_emb_CAA59487_ (X85230) peroxidase [Triticum aestivum]
Seq. No.	33496
Contig ID	328849_2.R1040
5'-most EST	jC-gmro02910074c05d1
Seq. No.	33497
Contig ID	328879_1.R1040
5'-most EST	jC-gmro02910013e08a1
Method	BLASTX
NCBI GI	g2851577
BLAST score	887
E value	8.0e-96
Match length	229
% identity	69
NCBI Description	SERINE CARBOXYPEPTIDASE III PRECURSOR (CP-MIII) >gi_1877219_emb_CAA70817_ (Y09604) serine carboxypeptidase III, CP-MIII [Hordeum vulgare]
Seq. No.	33498
Contig ID	328933_1.R1040
5'-most EST	uC-gmropic025h11b1
Method	BLASTX
NCBI GI	g2464901
BLAST score	263
E value	9.0e-23
Match length	79

% identity 70
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 33499
Contig ID 328993_1.R1040
5'-most EST jC-gmst02400020dc08d1
Method BLASTX
NCBI GI g3928097
BLAST score 216
E value 3.0e-17
Match length 88
% identity 49
NCBI Description (AC005770) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No. 33500
Contig ID 329011_1.R1040
5'-most EST uC-gmronoir030d10b1
Method BLASTX
NCBI GI g1888357
BLAST score 359
E value 5.0e-34
Match length 83
% identity 77
NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]
>gi_1890154_emb_CAA72432 (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No. 33501
Contig ID 329059_1.R1040
5'-most EST jC-gmro02910015a06d1

Seq. No. 33502
Contig ID 329077_1.R1040
5'-most EST jC-gmro02910015c10d1
Method BLASTX
NCBI GI g3377507
BLAST score 525
E value 2.0e-53
Match length 119
% identity 87
NCBI Description (AF056026) auxin transport protein EIR1 [Arabidopsis thaliana] >gi_3661620 (AF093241) putative auxin efflux carrier AGR [Arabidopsis thaliana] >gi_3746886 (AF087459) polar-auxin-transport efflux component AGRAVITROPIC 1 [Arabidopsis thaliana] >gi_4206709 (AF086906) root gravitropism control protein [Arabidopsis thaliana]

Seq. No. 33503
Contig ID 329171_1.R1040
5'-most EST jC-gmro02910016c04a1
Method BLASTX
NCBI GI g3334667
BLAST score 349
E value 1.0e-38
Match length 118
% identity 70

Contig ID	329460_1.R1040
5'-most EST	jC-gmro02910020e09d1
Seq. No.	33512
Contig ID	329587_1.R1040
5'-most EST	g4397439
Method	BLASTX
NCBI GI	g2244915
BLAST score	164
E value	2.0e-20
Match length	146
% identity	36
NCBI Description	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
Seq. No.	33513
Contig ID	329690_1.R1040
5'-most EST	jC-gmro02910022f05d1
Seq. No.	33514
Contig ID	329775_1.R1040
5'-most EST	jC-gmro02910022f10a1
Seq. No.	33515
Contig ID	329828_1.R1040
5'-most EST	jC-gmro02910023a08a1
Seq. No.	33516
Contig ID	329830_1.R1040
5'-most EST	jC-gmro02910023b08a1
Seq. No.	33517
Contig ID	329919_1.R1040
5'-most EST	jC-gmro02910023f03d1
Seq. No.	33518
Contig ID	330002_1.R1040
5'-most EST	jC-gmro02910024b08d1
Seq. No.	33519
Contig ID	330066_1.R1040
5'-most EST	jC-gmro02910024f10a1
Method	BLASTX
NCBI GI	g3395431
BLAST score	340
E value	7.0e-32
Match length	92
% identity	68
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.	33520
Contig ID	330120_1.R1040
5'-most EST	jC-gmro02910051h03d1
Seq. No.	33521
Contig ID	330137_1.R1040
5'-most EST	jC-gmro02910025a04a1

5'-most EST jC-gmro02910031f10d1
 Method BLASTX
 NCBI GI g3122572
 BLAST score 209
 E value 1.0e-16
 Match length 93
 % identity 53
 NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR
 (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I
 SUBUNIT) >gi_1084434_pir_S52737 NADH dehydrogenase
 (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato
 >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial
 complex I subunit [Solanum tuberosum]

Seq. No. 33540
 Contig ID 330842_1.R1040
 5'-most EST jC-gmro02910032e01d1
 Method BLASTX
 NCBI GI g4417296
 BLAST score 219
 E value 9.0e-18
 Match length 55
 % identity 67
 NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]

Seq. No. 33541
 Contig ID 330978_1.R1040
 5'-most EST jC-gmro02910034e02d1

Seq. No. 33542
 Contig ID 330988_1.R1040
 5'-most EST jC-gmro02910034e08d1
 Method BLASTN
 NCBI GI g1370197
 BLAST score 55
 E value 4.0e-22
 Match length 235
 % identity 87
 NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB8E

Seq. No. 33543
 Contig ID 330996_1.R1040
 5'-most EST jC-gmro02910034f02d1

Seq. No. 33544
 Contig ID 331016_1.R1040
 5'-most EST jC-gmro02910034g05d1

Seq. No. 33545
 Contig ID 331041_1.R1040
 5'-most EST jC-gmro02910071a10d1

Seq. No. 33546
 Contig ID 331077_1.R1040
 5'-most EST g4260395
 Method BLASTX
 NCBI GI g4220541

Seq. No. 33553
Contig ID 331526_1.R1040
5'-most EST uC-gmropic057a04b1

Seq. No. 33554
Contig ID 331534_1.R1040
5'-most EST jC-gmro02910039e10d1

Seq. No. 33555
Contig ID 331667_1.R1040
5'-most EST fC-gmro700864430d3

Seq. No. 33556
Contig ID 331711_1.R1040
5'-most EST jC-gmro02910040h10d1
Method BLASTX
NCBI GI g1771160
BLAST score 249
E value 3.0e-21
Match length 68
% identity 72
NCBI Description (X98929) SBT1 [*Lycopersicon esculentum*]
>gi_3687305_emb_CAA06999_ (AJ006378) subtilisin-like
protease [*Lycopersicon esculentum*]

Seq. No. 33557
Contig ID 331718_1.R1040
5'-most EST g4396669
Method BLASTX
NCBI GI g1354510
BLAST score 364
E value 1.0e-34
Match length 88
% identity 80
NCBI Description (U55205) HAL2-like protein [*Arabidopsis thaliana*]

Seq. No. 33558
Contig ID 331728_1.R1040
5'-most EST g5057699

Seq. No. 33559
Contig ID 331748_1.R1040
5'-most EST jC-gmro02910041021a1

Seq. No. 33560
Contig ID 331900_1.R1040
5'-most EST jC-gmro02910046b11d1

Seq. No. 33561
Contig ID 331913_1.R1040
5'-most EST jC-gmro02910046c07d1
Method BLASTX
NCBI GI g2961357
BLAST score 1217
E value 1.0e-134
Match length 322


```

% identity      73
NCBI Description (AL022140) putative protein [Arabidopsis thaliana]

Seq. No.        33562
Contig ID       332021_1.R1040
5'-most EST     jC-gmro02910047a02d1

Seq. No.        33563
Contig ID       332047_1.R1040
5'-most EST     jC-gmro02910047g02d1

Seq. No.        33564
Contig ID       332068_1.R1040
5'-most EST     jC-gmro02910068f04d1

Seq. No.        33565
Contig ID       332071_1.R1040
5'-most EST     jC-gmro02910047e02a1
Method          BLASTX
NCBI GI         g1888357
BLAST score     742
E value         7.0e-79
Match length    200
% identity      69
NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]
>gi_1890154_emb_CAA72432_(Y11767) alpha-mannosidase
precursor [Arabidopsis thaliana]

Seq. No.        33566
Contig ID       332107_1.R1040
5'-most EST     jC-gmro02910047h04a1

Seq. No.        33567
Contig ID       332126_1.R1040
5'-most EST     uC-gmropic074e11b1

Seq. No.        33568
Contig ID       332170_1.R1040
5'-most EST     jC-gmro02910048e03d1

Seq. No.        33569
Contig ID       332193_1.R1040
5'-most EST     jC-gmro02910048f09d1

Seq. No.        33570
Contig ID       332201_1.R1040
5'-most EST     jC-gmro02910048g03d1

Seq. No.        33571
Contig ID       332231_1.R1040
5'-most EST     jC-gmro02910049a07d1

Seq. No.        33572
Contig ID       332266_1.R1040
5'-most EST     jC-gmst02400031e03d1

Seq. No.        33573

```


Method	BLASTX
NCBI GI	g4006856
BLAST score	442
E value	1.0e-43
Match length	163
% identity	30
NCBI Description	(Z99707) receptor kinase-like protein [Arabidopsis thaliana]
Seq. No.	33597
Contig ID	334082_1.R1040
5'-most EST	fC-gmle700555604r2
Seq. No.	33598
Contig ID	334096_1.R1040
5'-most EST	jC-gmro02910069d07a1
Seq. No.	33599
Contig ID	334123_1.R1040
5'-most EST	jC-gmro02910069f07a1
Method	BLASTN
NCBI GI	g3510347
BLAST score	52
E value	4.0e-20
Match length	92
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.	33600
Contig ID	334151_1.R1040
5'-most EST	jC-gmro02910069h10d1
Method	BLASTX
NCBI GI	g1491617
BLAST score	270
E value	1.0e-23
Match length	82
% identity	67
NCBI Description	(X99952) peroxidase [Arabidopsis thaliana]
Seq. No.	33601
Contig ID	334213_1.R1040
5'-most EST	jC-gmro02910071h04a1
Seq. No.	33602
Contig ID	334269_1.R1040
5'-most EST	jC-gmro02910071a12d1
Method	BLASTX
NCBI GI	g2262111
BLAST score	194
E value	9.0e-15
Match length	76
% identity	50
NCBI Description	(AC002343) ribitol dehydrogenase isolog [Arabidopsis thaliana]
Seq. No.	33603

[Arabidopsis thaliana]

Seq. No.	33621
Contig ID	335427_1.R1040
5'-most EST	jC-gmst02400020db06d1
Seq. No.	33622
Contig ID	335428_1.R1040
5'-most EST	jC-gmst02400006g01a1
Seq. No.	33623
Contig ID	335429_1.R1040
5'-most EST	jC-gmst02400006g01d1
Seq. No.	33624
Contig ID	335484_1.R1040
5'-most EST	jC-gmst02400007b09d1
Method	BLASTX
NCBI GI	g3256035
BLAST score	202
E value	1.0e-15
Match length	77
% identity	49
NCBI Description	(Y14274) putative serine/threonine protein kinase [Sorghum bicolor]
Seq. No.	33625
Contig ID	335487_1.R1040
5'-most EST	fC-gmro700566572d3
Seq. No.	33626
Contig ID	335507_1.R1040
5'-most EST	jC-gmst02400007d07d1
Seq. No.	33627
Contig ID	335541_1.R1040
5'-most EST	jC-gmst02400007f07a1
Seq. No.	33628
Contig ID	335557_1.R1040
5'-most EST	jC-gmst02400007g09d1
Seq. No.	33629
Contig ID	335564_1.R1040
5'-most EST	jC-gmst02400007h05d1
Method	BLASTX
NCBI GI	g2098575
BLAST score	185
E value	1.0e-13
Match length	44
% identity	75
NCBI Description	(AC002115) F25451_2 [Homo sapiens]
Seq. No.	33630
Contig ID	335572_1.R1040
5'-most EST	jC-gmst02400077e05d1

E value	5.0e-19
Match length	64
% identity	66
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]
Seq. No.	33648
Contig ID	336562_1.R1040
5'-most EST	jC-gmst02400068f05d1
Seq. No.	33649
Contig ID	336593_1.R1040
5'-most EST	jC-gmst02400033h01d1
Seq. No.	33650
Contig ID	336627_2.R1040
5'-most EST	jC-gmst02400018c09a1
Seq. No.	33651
Contig ID	336637_1.R1040
5'-most EST	uC-gmr0noir008c11b1
Seq. No.	33652
Contig ID	336699_1.R1040
5'-most EST	jC-gmst02400045e10a1
Method	BLASTX
NCBI GI	g2980790
BLAST score	156
E value	3.0e-10
Match length	101
% identity	44
NCBI Description	(AL022197) hypothetical protein [Arabidopsis thaliana]
Seq. No.	33653
Contig ID	336781_1.R1040
5'-most EST	jC-gmst02400020de04d1
Seq. No.	33654
Contig ID	336789_1.R1040
5'-most EST	jC-gmst02400020f02a1
Seq. No.	33655
Contig ID	336855_1.R1040
5'-most EST	g5752695
Seq. No.	33656
Contig ID	336859_1.R1040
5'-most EST	jC-gmst02400045g09d1
Seq. No.	33657
Contig ID	336900_1.R1040
5'-most EST	jC-gmst02400023d09d1
Seq. No.	33658
Contig ID	336944_1.R1040
5'-most EST	jC-gmst02400023f03a1
Method	BLASTX
NCBI GI	q4454056

Contig ID	337441_1.R1040
5'-most EST	uC-gmrominsoy093h12b1
Method	BLASTX
NCBI GI	g3298544
BLAST score	452
E value	8.0e-45
Match length	201
% identity	57
NCBI Description	(AC004681) unknown protein [Arabidopsis thaliana]
Seq. No.	33667
Contig ID	337446_1.R1040
5'-most EST	jC-gmst02400027h03a1
Seq. No.	33668
Contig ID	337465_1.R1040
5'-most EST	jC-gmst02400028b05a1
Seq. No.	33669
Contig ID	337503_1.R1040
5'-most EST	jC-gmst02400028d10a1
Method	BLASTX
NCBI GI	g3702340
BLAST score	375
E value	9.0e-36
Match length	215
% identity	39
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]
Seq. No.	33670
Contig ID	337613_1.R1040
5'-most EST	jC-gmst02400029e01a1
Method	BLASTX
NCBI GI	g3776559
BLAST score	699
E value	6.0e-74
Match length	165
% identity	77
NCBI Description	(AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]
Seq. No.	33671
Contig ID	337662_1.R1040
5'-most EST	g5677286
Seq. No.	33672
Contig ID	337706_1.R1040
5'-most EST	jC-gmst02400030a12a1
Seq. No.	33673
Contig ID	337708_1.R1040
5'-most EST	jC-gmst02400030b01a1
Seq. No.	33674
Contig ID	337710_1.R1040

09684016

Seq. No.	33676
Contig ID	337763_1.R1040
5'-most EST	jC-qmst02400030q04d1

Method	BLASTN
NCBI GI	g747979
BLAST score	35

Match length	47
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NCBI Description Nicotiana tabacum UMP synthase (pyr5-6) mRNA, partial cds

Seq. No.	33679
Contig ID	337951_1.R1040
5'-most EST	jC-qmst02400032b03d1

Match length	97
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```
% identity 47
```

NCBI Description (AF058826) contains similarity to pseudouridylate synthases [Arabidopsis thaliana]

Seq. No.	33681
Contig ID	338060_1.R1040
5'-most EST	jC-qmst02400032h07d1

Seq. No.	33682
Contig ID	338065_1.R1040
5'-most EST	jC-qmst02400032h12d1

Seq. No.	33683
Contig ID	338082_1.R1040
5'-most EST	jC-qmst02400033a08d1

Seq. No.	33684
Contig ID	338091_1.R1040
5'-most EST	jC-qmst02400033b03d1

Seq. No.	33685
Contig ID	338112_1.R1040
5'-most EST	jC-gmst02400033c05d1
Seq. No.	33686
Contig ID	338180_1.R1040
5'-most EST	jC-gmst02400033g03d1
Seq. No.	33687
Contig ID	338188_1.R1040
5'-most EST	jC-gmst02400033g08d1
Seq. No.	33688
Contig ID	338192_1.R1040
5'-most EST	jC-gmst02400033g12d1
Method	BLASTN
NCBI GI	g499067
BLAST score	265
E value	1.0e-147
Match length	301
% identity	97
NCBI Description	G.max gmr2 gene
Seq. No.	33689
Contig ID	338204_1.R1040
5'-most EST	jC-gmst02400033h08a1
Seq. No.	33690
Contig ID	338269_1.R1040
5'-most EST	jC-gmst02400036a11d2
Seq. No.	33691
Contig ID	338281_1.R1040
5'-most EST	jC-gmst02400036b11d2
Seq. No.	33692
Contig ID	338526_1.R1040
5'-most EST	jC-gmst02400040b12a1
Seq. No.	33693
Contig ID	338748_1.R1040
5'-most EST	jC-gmst02400049e08d1
Seq. No.	33694
Contig ID	338812_1.R1040
5'-most EST	jC-gmst02400043h05d1
Seq. No.	33695
Contig ID	338830_1.R1040
5'-most EST	jC-gmst02400044a06a1
Seq. No.	33696
Contig ID	338831_1.R1040
5'-most EST	jC-gmst02400044a06d1
Seq. No.	33697
Contig ID	338843_1.R1040

NCBI GI g3335339
 BLAST score 161
 E value 8.0e-11
 Match length 106
 % identity 36
 NCBI Description (AC004512) Contains similarity to MADS-box protein AGL3 gb_U81369 from *A. thaliana*. [*Arabidopsis thaliana*]

Seq. No. 33715
 Contig ID 340137_1.R1040
 5'-most EST uC-gmropic008e06b1
 Method BLASTN
 NCBI GI g2598656
 BLAST score 52
 E value 3.0e-20
 Match length 100
 % identity 93
 NCBI Description *Vicia faba* mRNA for elongation factor 1-alpha (EF1-a)

Seq. No. 33716
 Contig ID 340162_1.R1040
 5'-most EST g4396083

Seq. No. 33717
 Contig ID 340366_1.R1040
 5'-most EST g5509055

Seq. No. 33718
 Contig ID 340398_1.R1040
 5'-most EST jC-gmst02400056f04a1
 Method BLASTX
 NCBI GI g818849
 BLAST score 599
 E value 4.0e-62
 Match length 161
 % identity 67
 NCBI Description (U25430) nucleotide pyrophosphatase precursor [*Oryza sativa*]

Seq. No. 33719
 Contig ID 340450_1.R1040
 5'-most EST jC-gmst02400057a05d1

Seq. No. 33720
 Contig ID 340520_1.R1040
 5'-most EST jC-gmst02400057d11d1

Seq. No. 33721
 Contig ID 340629_1.R1040
 5'-most EST jC-gmst02400058b05a1
 Method BLASTN
 NCBI GI g4567193
 BLAST score 39
 E value 1.0e-12
 Match length 202
 % identity 85
 NCBI Description *Arabidopsis thaliana* chromosome II BAC T26C19 genomic

[illegible]

```
Seq. No.          33723
Contig ID         340682_1.R1040
5'-most EST      jC-gmst02400058e06d1
Method            BLASTX
NCBI GI           g3023721
BLAST score       196
E value           8.0e-15
Match length      114
% identity        39
```

```
Seq. No.          33724
Contig ID         340719_1.R1040
5'-most EST      jC-gmst02400058h01a1
Method            BLASTX
NCBI GI           g112717
BLAST score       155
E value           4.0e-10
Match length      53
% identity        62
```

```
Seq. No.      33725
Contig ID     340790_1.R1040
5'-most EST   jC-gmst_02400060b05d1
```

Seq. No.	33727
Contig ID	341021_1.R1040
5'-most EST	fC-qmst700892334r4

Seq. No.	33728
Contig ID	341035_1.R1040
5'-most EST	jC-gmst02400062a10d1

```
Seq. No.      33729
Contig ID     341095_1.R1040
5'-most EST   jC-gmst02400062e10d1
```

```
Seq. No.          33730
Contig ID         341111_1.R1040
5'-most EST      jC-gmst02400062f10a1
```



```
Seq. No.          33731
Contig ID         341174_1.R1040
5'-most EST      jC-gmst02400063b01d1
```

```
Seq. No.      33732
Contig ID     341201_1.R1040
5'-most EST   jC-gmst02400063c06a1
```

```

Seq. No.          33733
Contig ID         341299_1.R1040
5'-most EST      jC-gmst02400063h08a1
Method            BLASTN
NCBI GI           g4567259
BLAST score       40
E value           5.0e-13
Match length      68
% identity        90
NCBI Description  Arabidopsis thaliana chromosome II BAC F3K23 genomic
                  sequence, complete sequence

```

```
Seq. No.          33734
Contig ID         341349_1.R1040
5'-most EST      jC-gmst02400064d10d1
Method            BLASTX
NCBI GI           g4049344
BLAST score       172
E value           3.0e-12
Match length      56
% identity        66
NCBI Description  (AL034567) putative protein [Arabidopsis thaliana]
```

```
Seq. No.          33735
Contig ID         341396_1.R1040
5'-most EST      jC-qmst02400065a07a2
```

```
Seq. No.          33736
Contig ID         341417_1.R1040
5'-most EST      jC-gmst02400065b09a2
Method            BLASTX
NCBI GI           g2062174
BLAST score       253
E value           1.0e-21
Match length      53
% identity        87
NCBI Description  (AC001645) transcription factor (TINY) isolog [Arabidopsis
                  thaliana]
```

```
Seq. No.          33737
Contig ID         341444_1.R1040
5'-most EST      jC-gmst02400065d01d1
Method            BLASTX
NCBI GI           g1076531
BLAST score       325
E value           6.0e-30
Match length      64
% identity        89
NCBI Description  hypothetical protein, pollen allergen homolog - garden pea
```


Seq. No. 33772
 Contig ID 343566_1.R1040
 5'-most EST fC-gmfl700904815r2

Seq. No. 33773
 Contig ID 343839_1.R1040
 5'-most EST fC-gmro700867181r5

Seq. No. 33774
 Contig ID 343856_1.R1040
 5'-most EST fC-gmfl700906093r5

Seq. No. 33775
 Contig ID 343870_1.R1040
 5'-most EST fC-gmfl700906121r2

Seq. No. 33776
 Contig ID 343881_1.R1040
 5'-most EST fC-gmfl700906134r2

Seq. No. 33777
 Contig ID 343895_1.R1040
 5'-most EST fC-gmfl700906171r2

Seq. No. 33778
 Contig ID 343916_1.R1040
 5'-most EST fC-gmfl700906377r2

Seq. No. 33779
 Contig ID 343927_1.R1040
 5'-most EST fC-gmfl700906435r2

Seq. No. 33780
 Contig ID 343938_1.R1040
 5'-most EST fC-gmfl700906442r6

Seq. No. 33781
 Contig ID 344084_1.R1040
 5'-most EST fC-gmle7000740015d1

Seq. No. 33782
 Contig ID 344112_1.R1040
 5'-most EST fC-gmle7000740866r1
 Method BLASTX
 NCBI GI g4115914
 BLAST score 389
 E value 2.0e-37
 Match length 109
 % identity 64

NCBI Description (AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=297.8, E=1.3e-85, N=1) [Arabidopsis thaliana] >gi_4539410_emb_CAB40043.1 (AL049524) putative Fe(II)/ascorbate oxidase [Arabidopsis thaliana]

Seq. No. 33783
 Contig ID 344116_1.R1040

SECRET

```
Seq. No.          33785
Contig ID         344207_1.R1040
5'-most EST      fC-gmse700758907a2
Method            BLASTX
NCBI GI           g2569940
BLAST score       302
E value           2.0e-27
Match length      132
% identity        49
NCBI Description  (Y15194) GRS protein [Arabidopsis thaliana]
```

```
Seq. No.          33787
Contig ID         344285_1.R1040
5'-most EST      fC-gmle7000763827r1
Method            BLASTX
NCBI GI           g3192042
BLAST score       283
E value           3.0e-25
Match length      111
% identity        55
NCBI Description  (AL023796) phosphoglucomutase [Schizosaccharomyces pombe]
```

```
Seq. No.          33788
Contig ID         344313_1.R1040
5'-most EST      fC-gmle700786228d4
Method            BLASTX
NCBI GI           g1076269
BLAST score       182
E value           3.0e-13
Match length      56
% identity        57
NCBI Description  pullulanase - spinach >gi_634093_emb_CAA58803_ (X83969)
                  pullulanase [Spinacia oleracea]
```

```
Seq. No.          33789
Contig ID         344347_1.R1040
5'-most EST      fC-gmro700567008r2
Method            BLASTX
NCBI GI           gl155255
BLAST score       340
E value           8.0e-32
Match length      119
% identity        57
NCBI Description  (U39228) beta-glucosidase [Prunus avium]
```

5102

Contig ID	345030_2.R1040
5'-most EST	fC-gmle700740810r4
Seq. No.	33815
Contig ID	345036_1.R1040
5'-most EST	fC-gmle700740866r4
Seq. No.	33816
Contig ID	345052_1.R1040
5'-most EST	fC-gmle700741226r3
Seq. No.	33817
Contig ID	345063_1.R1040
5'-most EST	fC-gmle700741294r3
Seq. No.	33818
Contig ID	345076_1.R1040
5'-most EST	fC-gmle700741539r4
Seq. No.	33819
Contig ID	345085_1.R1040
5'-most EST	fC-gmle700741958r3
Seq. No.	33820
Contig ID	345091_1.R1040
5'-most EST	fC-gmle700741988r4
Seq. No.	33821
Contig ID	345100_1.R1040
5'-most EST	fC-gmle700742139r4
Seq. No.	33822
Contig ID	345109_1.R1040
5'-most EST	fC-gmle700742323r4
Seq. No.	33823
Contig ID	345156_1.R1040
5'-most EST	fC-gmle700743339r4
Seq. No.	33824
Contig ID	345165_1.R1040
5'-most EST	fC-gmle700743470r3
Seq. No.	33825
Contig ID	345172_1.R1040
5'-most EST	fC-gmle700743611r4
Seq. No.	33826
Contig ID	345178_1.R1040
5'-most EST	fC-gmle700743613r3
Seq. No.	33827
Contig ID	345185_1.R1040
5'-most EST	fC-gmle700743672r3
Seq. No.	33828
Contig ID	345192_1.R1040

5'-most EST	fc-gmle700743681r3
Seq. No.	33829
Contig ID	345202_1.R1040
5'-most EST	fc-gmle700743719r3
Seq. No.	33830
Contig ID	345214_1.R1040
5'-most EST	fc-gmle700744058r4
Seq. No.	33831
Contig ID	345248_1.R1040
5'-most EST	fc-gmse7000763420d1
Seq. No.	33832
Contig ID	345275_1.R1040
5'-most EST	fc-gmle700787001d6
Method	BLASTN
NCBI GI	g3334860
BLAST score	125
E value	8.0e-64
Match length	310
% identity	91
NCBI Description	Solanum tuberosum chloroplast tRNA-Asn, tRNA-Arg genes
Seq. No.	33833
Contig ID	345286_1.R1040
5'-most EST	fc-gmse700787220d1
Seq. No.	33834
Contig ID	345303_1.R1040
5'-most EST	fc-gmle700788580r2
Seq. No.	33835
Contig ID	345312_1.R1040
5'-most EST	fc-gmst700891395r2
Seq. No.	33836
Contig ID	345314_1.R1040
5'-most EST	fc-gmle700789620d3
Method	BLASTX
NCBI GI	g3063691
BLAST score	133
E value	4.0e-18
Match length	81
% identity	54
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]
Seq. No.	33837
Contig ID	345359_1.R1040
5'-most EST	fc-gmst700892015d3
Seq. No.	33838
Contig ID	345412_1.R1040
5'-most EST	fc-gmle700872274d7
Seq. No.	33839

NCBI Description. HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION
>gi_539221_pir_S38045 hypothetical protein YKL207w - yeast
(Saccharomyces cerevisiae) >gi_486369_emb_CAA82052_
(Z28207) ORF YKL207w [Saccharomyces cerevisiae]

Seq. No. 33855
Contig ID 345904_1.R1040
5'-most EST fC-gmro700561429d7

Seq. No. 33856
Contig ID 346038_1.R1040
5'-most EST g5666824
Method BLASTX
NCBI GI g3879918
BLAST score 162
E value 4.0e-11
Match length 62
% identity 50
NCBI Description (Z74043) Similarity to Human beta-galactosidase
(SW:BGAL_HUMAN) [Caenorhabditis elegans]

Seq. No. 33857
Contig ID 346064_1.R1040
5'-most EST fC-gmro700565227r2

Seq. No. 33858
Contig ID 346103_1.R1040
5'-most EST fC-gmro700565834r2

Seq. No. 33859
Contig ID 346127_1.R1040
5'-most EST fC-gmro700566777r1
Method BLASTN
NCBI GI g971167
BLAST score 164
E value 4.0e-87
Match length 256
% identity 91
NCBI Description Pisum sativum Wando ornithine carbamoyltransferase mRNA,
complete cds

Seq. No. 33860
Contig ID 346207_1.R1040
5'-most EST fC-gmro700568583g1
Method BLASTX
NCBI GI g4490310
BLAST score 1256
E value 1.0e-143
Match length 313
% identity 82
NCBI Description (AL035678) somatic embryogenesis receptor-like kinase-like
protein [Arabidopsis thaliana]

Seq. No. 33861
Contig ID 346248_1.R1040
5'-most EST fC-gmro700744202r4

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Contig ID 346343_1.R1040
5'-most EST fC-gmro700746240r3

Seq. No. 33877
Contig ID 346362_1.R1040
5'-most EST fC-gmro700746472r4

Seq. No. 33878
Contig ID 346366_1.R1040
5'-most EST fC-gmro700746535r3

Seq. No. 33879
Contig ID 346372_1.R1040
5'-most EST fC-gmro700746614r3

Seq. No. 33880
Contig ID 346378_1.R1040
5'-most EST fC-gmro700746693r3

Seq. No. 33881
Contig ID 346383_1.R1040
5'-most EST fC-gmro700746706r3

Seq. No. 33882
Contig ID 346405_1.R1040
5'-most EST fC-gmro700746951r3

Seq. No. 33883
Contig ID 346414_1.R1040
5'-most EST fC-gmro700747038r4

Seq. No. 33884
Contig ID 346425_1.R1040
5'-most EST fC-gmro700747183r3

Seq. No. 33885
Contig ID 346431_1.R1040
5'-most EST fC-gmro700747276r3

Seq. No. 33886
Contig ID 346437_1.R1040
5'-most EST fC-gmro700747310r4

Seq. No. 33887
Contig ID 346443_1.R1040
5'-most EST fC-gmro700747348r3

Seq. No. 33888
Contig ID 346448_1.R1040
5'-most EST fC-gmro700747359r4

Seq. No. 33889
Contig ID 346458_1.R1040
5'-most EST fC-gmro700747479r4

Seq. No. 33890
Contig ID 346463_1.R1040

5'-most EST	fC-gmr0700747514r4
Seq. No.	33891
Contig ID	346468_1.R1040
5'-most EST	fC-gmr0700747557r4
Seq. No.	33892
Contig ID	346477_1.R1040
5'-most EST	fC-gmr0700747701r3
Seq. No.	33893
Contig ID	346483_1.R1040
5'-most EST	fC-gmr0700747711r3
Seq. No.	33894
Contig ID	346494_1.R1040
5'-most EST	fC-gmr0700747787r3
Seq. No.	33895
Contig ID	346504_1.R1040
5'-most EST	fC-gmr0700748151r4
Seq. No.	33896
Contig ID	346509_1.R1040
5'-most EST	fC-gmr0700748156r4
Seq. No.	33897
Contig ID	346513_1.R1040
5'-most EST	fC-gmr0700748208r3
Seq. No.	33898
Contig ID	346518_1.R1040
5'-most EST	fC-gmr0700748236r4
Seq. No.	33899
Contig ID	346523_1.R1040
5'-most EST	fC-gmr0700748271r3
Seq. No.	33900
Contig ID	346528_1.R1040
5'-most EST	fC-gmr0700748296r3
Seq. No.	33901
Contig ID	346533_1.R1040
5'-most EST	fC-gmr0700748342r4
Seq. No.	33902
Contig ID	346537_1.R1040
5'-most EST	fC-gmr0700748409r3
Seq. No.	33903
Contig ID	346552_1.R1040
5'-most EST	fC-gmr0700748540r3
Seq. No.	33904
Contig ID	346558_1.R1040
5'-most EST	fC-gmr0700748571r4

Seq. No.	33905
Contig ID	346562_1.R1040
5'-most EST	fC-gmr ^o 700748591r4
Seq. No.	33906
Contig ID	346571_1.R1040
5'-most EST	fC-gmr ^o 700748726r3
Seq. No.	33907
Contig ID	346576_1.R1040
5'-most EST	fC-gmr ^o 700748737r3
Seq. No.	33908
Contig ID	346581_1.R1040
5'-most EST	fC-gmr ^o 700748836r3
Seq. No.	33909
Contig ID	346587_1.R1040
5'-most EST	fC-gmr ^o 700748845r3
Seq. No.	33910
Contig ID	346596_1.R1040
5'-most EST	fC-gmr ^o 700749034r3
Seq. No.	33911
Contig ID	346602_1.R1040
5'-most EST	fC-gmr ^o 700749069r3
Seq. No.	33912
Contig ID	346612_1.R1040
5'-most EST	fC-gmr ^o 700749140r3
Seq. No.	33913
Contig ID	346618_1.R1040
5'-most EST	fC-gmr ^o 700749247r4
Seq. No.	33914
Contig ID	346627_1.R1040
5'-most EST	fC-gmr ^o 700749265r4
Seq. No.	33915
Contig ID	346632_1.R1040
5'-most EST	fC-gmr ^o 700749283r4
Seq. No.	33916
Contig ID	346637_1.R1040
5'-most EST	fC-gmr ^o 700749341r3
Seq. No.	33917
Contig ID	346643_1.R1040
5'-most EST	fC-gmr ^o 700749381r3
Seq. No.	33918
Contig ID	346648_1.R1040
5'-most EST	fC-gmr ^o 700749436r3

Contig ID	346756_1.R1040
5'-most EST	fC-gmro700792724r8
Seq. No.	33932
Contig ID	346787_1.R1040
5'-most EST	fC-gmro700795004f1
Seq. No.	33933
Contig ID	346806_1.R1040
5'-most EST	fC-gmro700795654r6
Seq. No.	33934
Contig ID	346878_1.R1040
5'-most EST	fC-gmro700834955g1
Method	BLASTX
NCBI GI	g3335351
BLAST score	579
E value	1.0e-59
Match length	179
% identity	12
NCBI Description	(AC004512) Similar to ERECTA receptor protein kinase gb_D83257 from A. thaliana. ESTs gb_T41629 and gb_AA586072 come from this gene. [Arabidopsis thaliana]
Seq. No.	33935
Contig ID	346885_1.R1040
5'-most EST	fC-gmro700835567e1
Seq. No.	33936
Contig ID	347090_1.R1040
5'-most EST	fC-gmro700844704d4
Method	BLASTX
NCBI GI	g3096919
BLAST score	721
E value	3.0e-76
Match length	206
% identity	78
NCBI Description	(AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	33937
Contig ID	347220_1.R1040
5'-most EST	fC-gmro700865409d3
Seq. No.	33938
Contig ID	347240_1.R1040
5'-most EST	fC-gmro700847173f2
Seq. No.	33939
Contig ID	347283_1.R1040
5'-most EST	fC-gmro700846785r4
Seq. No.	33940
Contig ID	347315_1.R1040
5'-most EST	fC-gmro700847042r7
Seq. No.	33941

Contig ID 347422_1.R1040
5'-most EST fC-gmro700848272r5

Seq. No. 33942
Contig ID 347579_1.R1040
5'-most EST fC-gmro700864412r5

Seq. No. 33943
Contig ID 347591_1.R1040
5'-most EST fC-gmst700791918r2

Seq. No. 33944
Contig ID 347611_1.R1040
5'-most EST fC-gmro700864858r5

Seq. No. 33945
Contig ID 347732_1.R1040
5'-most EST fC-gmro700865758r3

Seq. No. 33946
Contig ID 347908_1.R1040
5'-most EST fC-gmro700868363r3

Seq. No. 33947
Contig ID 348010_1.R1040
5'-most EST fC-gmst700890071d3
Method BLASTX
NCBI GI g886116
BLAST score 180
E value 3.0e-13
Match length 43
% identity 72
NCBI Description (U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473
(AF051338) xyloglucan endotransglycosylase related protein
[Arabidopsis thaliana]

Seq. No. 33948
Contig ID 348076_1.R1040
5'-most EST fC-gmro700873716d1

Seq. No. 33949
Contig ID 348077_1.R1040
5'-most EST fC-gmro700873747d1

Seq. No. 33950
Contig ID 348081_1.R1040
5'-most EST fC-gmst700891472r1

Seq. No. 33951
Contig ID 348300_1.R1040
5'-most EST fC-gmse7000752657r1
Method BLASTX
NCBI GI g2245131
BLAST score 209
E value 2.0e-16
Match length 89
% identity 51

NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 33952
 Contig ID 348319_1.R1040
 5'-most EST fC-gmse7000753191f1
 Method BLASTX
 NCBI GI g232161
 BLAST score 284
 E value 2.0e-25
 Match length 83
 % identity 69
 NCBI Description 19 KD GLOBULIN PRECURSOR (ALPHA-GLOBULIN)
 >gi_68857_pir_WMRZ19 19K globulin precursor - rice
 >gi_20159_emb_CAA45400_ (X63990) 19 kDa globulin precursor
 [Oryza sativa]

Seq. No. 33953
 Contig ID 348339_1.R1040
 5'-most EST fC-gmse700753764a1
 Method BLASTX
 NCBI GI g3608134
 BLAST score 388
 E value 3.0e-37
 Match length 253
 % identity 36
 NCBI Description (AC005314) dnaJ-like protein [Arabidopsis thaliana]

Seq. No. 33954
 Contig ID 348349_1.R1040
 5'-most EST fC-gmse700754105d2

Seq. No. 33955
 Contig ID 348371_1.R1040
 5'-most EST fC-gmse700754553d1

Seq. No. 33956
 Contig ID 348455_1.R1040
 5'-most EST fC-gmse700762414d3
 Method BLASTX
 NCBI GI g4469013
 BLAST score 347
 E value 1.0e-32
 Match length 122
 % identity 61
 NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No. 33957
 Contig ID 348562_1.R1040
 5'-most EST fC-gmse700758907d4

Seq. No. 33958
 Contig ID 348674_1.R1040
 5'-most EST fC-gmst700649675a3
 Method BLASTN
 NCBI GI g169752
 BLAST score 127
 E value 3.0e-65

[illegible]

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Seq. No.          33979
Contig ID         350110_1.R1040
5'-most EST      fC-gmst700665136r1
Method            BLASTX
NCBI GI           g4234955
BLAST score       210
E value           1.0e-16
Match length      80
% identity        51
NCBI Description  (AF098971) NBS-LRR
```

Seq. No.	33981
Contig ID	350190_1.R1040
5'-most EST	fC-qmse700672612z1

Seq. No.	33983
Contig ID	350257_1.R1040
5'-most EST	fC-qmse700673112r3

Seq. No.	33985
Contig ID	350661_1.R1040
5'-most EST	q5605669

Seq. No.	33987
Contig ID	350780_1.R1040
5'-most EST	fC-qmse700753037d4

5121

000001 91048950

5'-most EST	fC-gmst700651965d7
Seq. No.	34004
Contig ID	352072_1.R1040
5'-most EST	fC-gmst700653543r6
Method	BLASTX
NCBI GI	g861157
BLAST score	968
E value	1.0e-105
Match length	247
% identity	76
NCBI Description	(Z35163) cell wall invertase II; beta-furanofructosidase [Vicia faba]
Seq. No.	34005
Contig ID	352186_1.R1040
5'-most EST	fC-gmst700653794r7
Seq. No.	34006
Contig ID	352317_1.R1040
5'-most EST	fC-gmst700660827r5
Seq. No.	34007
Contig ID	352327_1.R1040
5'-most EST	fC-gmst700660854r5
Seq. No.	34008
Contig ID	352407_1.R1040
5'-most EST	fC-gmst700661765r3
Seq. No.	34009
Contig ID	352411_1.R1040
5'-most EST	fC-gmst700661785d4
Seq. No.	34010
Contig ID	352454_1.R1040
5'-most EST	fC-gmst700662075r5
Seq. No.	34011
Contig ID	352478_1.R1040
5'-most EST	fC-gmst700662785b1
Seq. No.	34012
Contig ID	352518_1.R1040
5'-most EST	fC-gmst700662684d3
Seq. No.	34013
Contig ID	352596_1.R1040
5'-most EST	fC-gmst700663510r3
Seq. No.	34014
Contig ID	352799_1.R1040
5'-most EST	fC-gmst700664577r3
Seq. No.	34015
Contig ID	353012_1.R1040
5'-most EST	fC-gmst700665233r6

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Seq. No. 34038
 Contig ID 354418_1.R1040
 5'-most EST g4302953

Seq. No. 34039
 Contig ID 354536_1.R1040
 5'-most EST uC-gmflminsoy014b10b1

Seq. No. 34040
 Contig ID 354555_1.R1040
 5'-most EST uC-gmrominsoy250c10b1
 Method BLASTX
 NCBI GI g2244971
 BLAST score 625
 E value 3.0e-65
 Match length 143
 % identity 87
 NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 34041
 Contig ID 354595_1.R1040
 5'-most EST uC-gmrominsoy0001h10b1
 Method BLASTX
 NCBI GI g4406820
 BLAST score 572
 E value 4.0e-59
 Match length 136
 % identity 77
 NCBI Description (AC006201) putative ras superfamily member [Arabidopsis thaliana]

Seq. No. 34042
 Contig ID 354599_1.R1040
 5'-most EST uC-gmflminsoy015c06b1
 Method BLASTX
 NCBI GI g3522943
 BLAST score 717
 E value 5.0e-76
 Match length 177
 % identity 38
 NCBI Description (AC004411) putative p-glycoprotein [Arabidopsis thaliana]

Seq. No. 34043
 Contig ID 354617_1.R1040
 5'-most EST uC-gmflminsoy016d06b1

Seq. No. 34044
 Contig ID 354659_1.R1040
 5'-most EST uC-gmropic096e06b1
 Method BLASTX
 NCBI GI g3947735
 BLAST score 313
 E value 1.0e-28
 Match length 139
 % identity 48
 NCBI Description (AJ009720) NL27 [Solanum tuberosum]

E value	2.0e-21
Match length	88
% identity	97
NCBI Description	Phaseolus vulgaris dehydrin mRNA, complete cds
Seq. No.	34077
Contig ID	356556_1.R1040
5'-most EST	g5605939
Seq. No.	34078
Contig ID	356709_1.R1040
5'-most EST	uC-gmflminsoy047h01b1
Seq. No.	34079
Contig ID	356715_1.R1040
5'-most EST	uC-gmflminsoy047h08b1
Seq. No.	34080
Contig ID	356770_1.R1040
5'-most EST	g4286721
Method	BLASTX
NCBI GI	g1362112
BLAST score	469
E value	3.0e-65
Match length	169
% identity	76
NCBI Description	protein kinase NPK2 (EC 2.7.1.-) - common tobacco >gi_862342_dbj_BAA06731_ (D31964) NPK2 [Nicotiana tabacum]
Seq. No.	34081
Contig ID	356863_1.R1040
5'-most EST	uC-gmropic092e11b1
Method	BLASTX
NCBI GI	g3068704
BLAST score	535
E value	2.0e-54
Match length	232
% identity	49
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]
Seq. No.	34082
Contig ID	356872_1.R1040
5'-most EST	uC-gmflminsoy053f11b1
Method	BLASTX
NCBI GI	g2245036
BLAST score	304
E value	2.0e-27
Match length	174
% identity	44
NCBI Description	(Z97342) triacylglycerol lipase homolog [Arabidopsis thaliana]
Seq. No.	34083
Contig ID	356943_1.R1040
5'-most EST	uC-gmflminsoy054e08b1
Seq. No.	34084

Contig ID 358703_1.R1040
 5'-most EST uC-gmflminsoy080d03b1
 Method BLASTX
 NCBI GI g2149640
 BLAST score 697
 E value 1.0e-73
 Match length 156
 % identity 84
 NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No. 34103
 Contig ID 358725_1.R1040
 5'-most EST uC-gmflminsoy080g08b1

Seq. No. 34104
 Contig ID 358731_1.R1040
 5'-most EST uC-gmronoir045a03b1
 Method BLASTX
 NCBI GI g1351676
 BLAST score 185
 E value 3.0e-30
 Match length 153
 % identity 43
 NCBI Description PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C21E11.05C
 >gi_2130307_pir_S62590 hypothetical protein SPAC21E11.05c
 - fission yeast (Schizosaccharomyces pombe)
 >gi_1067221_emb_CAA91964_(Z67999) peptidyl-prolyl
 cis-trans isomerase [Schizosaccharomyces pombe]

Seq. No. 34105
 Contig ID 358867_1.R1040
 5'-most EST uC-gmflminsoy082f08b1
 Method BLASTX
 NCBI GI g3283026
 BLAST score 343
 E value 4.0e-32
 Match length 173
 % identity 36
 NCBI Description (AF051562) putative transposase [Arabidopsis thaliana]

Seq. No. 34106
 Contig ID 358885_1.R1040
 5'-most EST g5607084

Seq. No. 34107
 Contig ID 358918_1.R1040
 5'-most EST uC-gmropic097g07b1
 Method BLASTX
 NCBI GI g3482972
 BLAST score 159
 E value 1.0e-10
 Match length 124
 % identity 32
 NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Seq. No. 34108
 Contig ID 358964_1.R1040

(EC 2.4.1.119) 50K chain - human

Seq. No. 34137
Contig ID 361222_1.R1040
5'-most EST uC-gmrominsoy062a10b1
Method BLASTX
NCBI GI g1184072
BLAST score 370
E value 1.0e-35
Match length 82
% identity 88
NCBI Description (U40766) COL-1 [Meloidogyne incognita]

Seq. No. 34138
Contig ID 361236_1.R1040
5'-most EST uC-gmrominsoy062c03b1

Seq. No. 34139
Contig ID 361259_1.R1040
5'-most EST uC-gmrominsoy090g08b1

Seq. No. 34140
Contig ID 361289_1.R1040
5'-most EST uC-gmrominsoy064b09b1
Method BLASTX
NCBI GI g547837
BLAST score 259
E value 2.0e-22
Match length 136
% identity 38
NCBI Description L-LACTATE DEHYDROGENASE >gi_480440_pir_S36863 L-lactate dehydrogenase (EC 1.1.1.27) - Thermotoga maritima
>gi_396281_emb_CAA52355_ (X74302) L-lactate dehydrogenase [Thermotoga maritima]

Seq. No. 34141
Contig ID 361298_1.R1040
5'-most EST uC-gmrominsoy174d09b1

Seq. No. 34142
Contig ID 361446_1.R1040
5'-most EST uC-gmrominsoy069b09b1
Method BLASTX
NCBI GI g2129698
BLAST score 168
E value 9.0e-12
Match length 59
% identity 53
NCBI Description protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana
>gi_1054633_emb_CAA63387_ (X92728) protein kinase [Arabidopsis thaliana]

Seq. No. 34143
Contig ID 361485_1.R1040
5'-most EST uC-gmrominsoy071f10b1
Method BLASTX
NCBI GI g3860249

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Contig ID	368656_1.R1040
5'-most EST	uC-gmrominsoy317b11b1
Seq. No.	34230
Contig ID	368700_1.R1040
5'-most EST	uC-gmrominsoy318c12b1
Method	BLASTN
NCBI GI	g16185
BLAST score	235
E value	1.0e-129
Match length	356
% identity	92
NCBI Description	A.thaliana atpgp1 gene for P-glycoprotein, homologous to mammalian mdm genes
Seq. No.	34231
Contig ID	368716_1.R1040
5'-most EST	uC-gmrominsoy318e06b1
Method	BLASTN
NCBI GI	g3738275
BLAST score	504
E value	0.0e+00
Match length	516
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	34232
Contig ID	368730_1.R1040
5'-most EST	uC-gmrominsoy318g09b1
Method	BLASTN
NCBI GI	g4006885
BLAST score	336
E value	0.0e+00
Match length	372
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No
Seq. No.	34233
Contig ID	368731_1.R1040
5'-most EST	uC-gmrominsoy318h12b1
Method	BLASTN
NCBI GI	g2244950
BLAST score	520
E value	0.0e+00
Match length	536
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	34234
Contig ID	368740_1.R1040
5'-most EST	uC-gmrominsoy318h09b1
Method	BLASTN
NCBI GI	g16473
BLAST score	507

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Seq. No.	34242
Contig ID	369144_1.R1040
5'-most EST	uC-gmronoir007g05b1
Method	BLASTX
NCBI GI	g2597972
BLAST score	513
E value	3.0e-52
Match length	124
% identity	71
NCBI Description	(AJ001621) RAL-1 protein [Litomosoides sigmodontis]
Seq. No.	34243
Contig ID	369169_1.R1040
5'-most EST	uC-gmronoir043b10b1
Method	BLASTX
NCBI GI	g1236781
BLAST score	308
E value	2.0e-28
Match length	95
% identity	65
NCBI Description	(X96732) cuticular collagen [Ostertagia circumcincta]
Seq. No.	34244
Contig ID	369195_1.R1040
5'-most EST	uC-gmronoir057h07b1
Seq. No.	34245
Contig ID	369200_1.R1040
5'-most EST	uC-gmronoir009b06b1
Seq. No.	34246
Contig ID	369208_1.R1040
5'-most EST	uC-gmronoir054b12b1
Seq. No.	34247
Contig ID	369215_1.R1040
5'-most EST	uC-gmronoir009e06b1
Method	BLASTX
NCBI GI	g2982452
BLAST score	247
E value	5.0e-21
Match length	147
% identity	6
NCBI Description	(AL022223) receptor protein kinase-like protein [Arabidopsis thaliana]
Seq. No.	34248
Contig ID	369217_1.R1040
5'-most EST	uC-gmronoir035g05b1
Method	BLASTX
NCBI GI	g2500025
BLAST score	318
E value	2.0e-29
Match length	127
% identity	46
NCBI Description	PROBABLE ADENYLOSUCCINATE SYNTHETASE (IMP--ASPARTATE LIGASE) >gi_1825781 (U88315) Similar to adenylosuccinate

synthetase; coded for by C. elegans cDNA yk104b12.3; coded for by C. elegans cDNA yk121e6.3; coded for by C. elegans cDNA yk117a11.3; coded for by C. elegans cDNA yk19c6.3; coded for by C. elegans cDNA yk

Seq. No. 34249
Contig ID 369219_1.R1040
5'-most EST uC-gmrñnoir054f03b1

Seq. No. 34250
Contig ID 369222_1.R1040
5'-most EST uC-gmrñnoir057g11b1
Method BLASTX
NCBI GI g3096951
BLAST score 471
E value 2.0e-47
Match length 103
% identity 90
NCBI Description (AJ005784) heat shock protein 90 [Brugia pahangi]

Seq. No. 34251
Contig ID 369307_1.R1040
5'-most EST uC-gmrñnoir033e09b1

Seq. No. 34252
Contig ID 369326_1.R1040
5'-most EST uC-gmrñnoir012h12b1
Method BLASTX
NCBI GI g1706582
BLAST score 747
E value 1.0e-79
Match length 149
% identity 95
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_1072161 (U40935) elongation-factor 1-alpha [Caenorhabditis elegans] >gi_1255296 (U51994) coded for by C. elegans cDNA CEESE09R; coded for by C. elegans cDNA CEESH59F; coded for by C. elegans cDNA CESAE06F; coded for by C. elegans cDNA yk1d11.3; coded for by C. elegans cDNA yk1d11.5; coded for by C. elegans cDNA yk17e7.3

Seq. No. 34253
Contig ID 369366_1.R1040
5'-most EST uC-gmrñnoir014a01b1

Seq. No. 34254
Contig ID 369430_1.R1040
5'-most EST uC-gmrñnoir040b12b1

Seq. No. 34255
Contig ID 369514_1.R1040
5'-most EST uC-gmrñnoir040d07b1

Seq. No. 34256
Contig ID 369567_1.R1040
5'-most EST uC-gmrñnoir052b03b1

Contig ID	370363_1.R1040
5'-most EST	uC-gmropic075b08b1
Seq. No.	34268
Contig ID	370443_1.R1040
5'-most EST	uC-gmronoir050c02b1
Seq. No.	34269
Contig ID	370734_1.R1040
5'-most EST	uC-gmronoir059a02b1
Seq. No.	34270
Contig ID	371053_1.R1040
5'-most EST	uC-gmronoir070e12b1
Seq. No.	34271
Contig ID	371095_1.R1040
5'-most EST	uC-gmronoir073c02b1
Seq. No.	34272
Contig ID	371263_1.R1040
5'-most EST	uC-gmropic0001h09a1
Seq. No.	34273
Contig ID	371706_1.R1040
5'-most EST	uC-gmropic014c01b1
Seq. No.	34274
Contig ID	371818_1.R1040
5'-most EST	uC-gmropic106g05b1
Seq. No.	34275
Contig ID	372045_1.R1040
5'-most EST	uC-gmropic015c03b1
Seq. No.	34276
Contig ID	372149_1.R1040
5'-most EST	uC-gmropic016g08b1
Method	BLASTX
NCBI GI	g1707017
BLAST score	533
E value	1.0e-54
Match length	115
% identity	90
NCBI Description	(U78721) RNA helicase isolog [Arabidopsis thaliana]
Seq. No.	34277
Contig ID	372556_1.R1040
5'-most EST	uC-gmropic022f01b1
Seq. No.	34278
Contig ID	373030_1.R1040
5'-most EST	uC-gmropic028g01b1
Method	BLASTX
NCBI GI	g3953471
BLAST score	563
E value	4.0e-58

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Seq. No.	34288
Contig ID	376035_1.R1040
5'-most EST	uC-gmropic073g03b1
Method	BLASTX
NCBI GI	g2959320
BLAST score	271
E value	9.0e-24
Match length	59
% identity	90
NCBI Description	(Z97057) ANR1 , MA

Seq. No.	34290
Contig ID	376082_1.R1040
5'-most EST	q957409

Seq. No.	34292
Contig ID	376326_1.R1040
5'-most EST	q5057783

Seq. No.	34294
Contig ID	376624_1.R1040
5'-most EST	uC-gmropic090h02b1

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Seq. No.          34296
Contig ID         377209_1.R1040
5'-most EST      uC-gmröpic102b02b1
Method            BLASTX
```


Method	BLASTX
NCBI GI	g1495804
BLAST score	442
E value	4.0e-44
Match length	110
% identity	75
NCBI Description	(X96406) 13-lipoxygenase [Solanum tuberosum]
Seq. No.	34304
Contig ID	378666_1.R1040
5'-most EST	g4260450
Seq. No.	34305
Contig ID	378715_1.R1040
5'-most EST	g4277028
Seq. No.	34306
Contig ID	379005_1.R1040
5'-most EST	g4292087
Method	BLASTX
NCBI GI	g3549691
BLAST score	1112
E value	1.0e-122
Match length	209
% identity	89
NCBI Description	(AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]
Seq. No.	34307
Contig ID	379147_1.R1040
5'-most EST	g5508921
Method	BLASTX
NCBI GI	g1170601
BLAST score	169
E value	6.0e-12
Match length	119
% identity	42
NCBI Description	FRUIT PROTEIN PKIWI502 >gi_1085869_pir_S48036 hypothetical protein - kiwi fruit >gi_450237 (L27809) pKIWI502 [Actinidia deliciosa]
Seq. No.	34308
Contig ID	379387_1.R1040
5'-most EST	g4290656
Seq. No.	34309
Contig ID	379614_1.R1040
5'-most EST	g4284382
Method	BLASTX
NCBI GI	g4580470
BLAST score	172
E value	9.0e-12
Match length	141
% identity	38
NCBI Description	(AC006081) hypothetical protein [Arabidopsis thaliana]
Seq. No.	34310
Contig ID	380046_1.R1040

% identity	49
NCBI Description	46 KD FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) >gi_1079010_pir_A55320 immunophilin FKBP46 - fall armyworm >gi_595845 (U15038) immunophilin FKBP46 [Spodoptera frugiperda]
Seq. No.	34321
Contig ID	381949_1.R1040
5'-most EST	g4307437
Method	BLASTX
NCBI GI	g3929383
BLAST score	152
E value	7.0e-10
Match length	71
% identity	45
NCBI Description	SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN) >gi_1405747_emb_CAA67134_ (X98511) PR264/SC35 [Mus musculus]
Seq. No.	34322
Contig ID	381980_1.R1040
5'-most EST	g4302233
Method	BLASTX
NCBI GI	g2500047
BLAST score	221
E value	6.0e-18
Match length	50
% identity	82
NCBI Description	SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_534916_emb_CAA85362_ (Z36894) soluble inorganic pyrophosphatase [Solanum tuberosum]
Seq. No.	34323
Contig ID	382296_1.R1040
5'-most EST	g4304627
Method	BLASTX
NCBI GI	g4580469
BLAST score	324
E value	4.0e-30
Match length	110
% identity	52
NCBI Description	(AC006081) putative zinc finger protein [Arabidopsis thaliana]
Seq. No.	34324
Contig ID	382950_1.R1040
5'-most EST	g4313493
Seq. No.	34325
Contig ID	383013_1.R1040
5'-most EST	g5605731
Seq. No.	34326
Contig ID	383813_1.R1040
5'-most EST	q5510237

Seq. No. 34358
Contig ID 389736 1.R1040
5'-most EST g5126906

Seq. No. 34359
Contig ID 390118 1.R1040
5'-most EST g5607175

Seq. No. 34360
Contig ID 390135 1.R1040
5'-most EST g5607195
Method BLASTX
NCBI GI g3176664
BLAST score 489
E value 4.0e-49
Match length 147
% identity 61
NCBI Description (AC004393) Contains similarity to beta scruin gb_Z47541 from *Limulus polyphemus*. ESTs gb_T04493 and gb_AA585955 come from this gene. [*Arabidopsis thaliana*]

Seq. No. 34361
Contig ID 390140 1.R1040
5'-most EST g5607200

Seq. No. 34362
Contig ID 390196 1.R1040
5'-most EST g5752876

Seq. No. 34363
Contig ID 390256 1.R1040
5'-most EST g5752967

Seq. No. 34364
Contig ID 390386 1.R1040
5'-most EST g5509519

Seq. No. 34365
Contig ID 390429 1.R1040
5'-most EST g5342384

Seq. No. 34366
Contig ID 390578 1.R1040
5'-most EST g5509632

Seq. No. 34367
Contig ID 390581 1.R1040
5'-most EST g5509635

Seq. No. 34368
Contig ID 390634 1.R1040
5'-most EST g5510190

Seq. No. 34369
Contig ID 390646 1.R1040
5'-most EST g5509650

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

5'-most EST	g5510310
Seq. No.	34379
Contig ID	391062 1.R1040
5'-most EST	g5509851
Seq. No.	34380
Contig ID	391100 1.R1040
5'-most EST	g5510049
Seq. No.	34381
Contig ID	391112 1.R1040
5'-most EST	g5677115
Method	BLASTX
NCBI GI	g2245026
BLAST score	223
E value	3.0e-18
Match length	62
% identity	66
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No.	34382
Contig ID	391131 1.R1040
5'-most EST	g5676954
Seq. No.	34383
Contig ID	391165 1.R1040
5'-most EST	g5510362
Seq. No.	34384
Contig ID	391177 1.R1040
5'-most EST	g5510366
Method	BLASTN
NCBI GI	g1304226
BLAST score	54
E value	1.0e-21
Match length	98
% identity	89
NCBI Description	Soybean mRNA for epoxide hydrolase, complete cds
Seq. No.	34385
Contig ID	391178 1.R1040
5'-most EST	g5510069
Seq. No.	34386
Contig ID	391205 1.R1040
5'-most EST	g5510395
Seq. No.	34387
Contig ID	391259 1.R1040
5'-most EST	g5676991
Seq. No.	34388
Contig ID	391956 1.R1040
5'-most EST	g5342392
Method	BLASTX
NCBI GI	q3688284

BLAST score 157
 E value 2.0e-10
 Match length 38
 % identity 79
 NCBI Description (AJ011567) lanatoside 15'-O-acetylerase [Digitalis lanata]

Seq. No. 34389
 Contig ID 392276_1.R1040
 5'-most EST g5677448

Seq. No. 34390
 Contig ID 392704_1.R1040
 5'-most EST g5677731

Seq. No. 34391
 Contig ID 392824_1.R1040
 5'-most EST g5678156
 Method BLASTN
 NCBI GI g2943791
 BLAST score 34
 E value 1.0e-09
 Match length 70
 % identity 87
 NCBI Description Cucurbita sp. mRNA for PV72, complete cds

Seq. No. 34392
 Contig ID 392855_1.R1040
 5'-most EST g5342437
 Method BLASTX
 NCBI GI g3482913
 BLAST score 560
 E value 1.0e-57
 Match length 171
 % identity 58
 NCBI Description (AC003970) Similar to MtN21, gi_2598575, Megicago truncatula nodulation induced gene [Arabidopsis thaliana]

Seq. No. 34393
 Contig ID 393033_1.R1040
 5'-most EST g5342645

Seq. No. 34394
 Contig ID 393085_1.R1040
 5'-most EST g5342660

Seq. No. 34395
 Contig ID 393712_1.R1040
 5'-most EST g5175420

Seq. No. 34396
 Contig ID 394354_1.R1040
 5'-most EST g5752568

Seq. No. 34397
 Seq. ID 2DA-01-Q1-B1-A4
 Method BLASTX

NCBI GI g1155090
 BLAST score 231
 E value 2.0e-19
 Match length 67
 % identity 61
 NCBI Description (X94986) beta glucosidase [Manihot esculenta]

Seq. No. 34398
 Seq. ID 2DA-01-Q1-B1-B2
 Method BLASTN
 NCBI GI g2264316
 BLAST score 51
 E value 4.0e-20
 Match length 82
 % identity 72
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No. 34399
 Seq. ID 2DA-01-Q1-B1-D3
 Method BLASTX
 NCBI GI g4539395
 BLAST score 415
 E value 6.0e-41
 Match length 112
 % identity 71
 NCBI Description (AL035526) putative protein [Arabidopsis thaliana]

Seq. No. 34400
 Seq. ID 2DA-01-Q1-B1-D5
 Method BLASTX
 NCBI GI g1495366
 BLAST score 207
 E value 1.0e-16
 Match length 99
 % identity 38
 NCBI Description (Z69370) nitrite transporter [Cucumis sativus]

Seq. No. 34401
 Seq. ID 2DA-01-Q1-B1-G11
 Method BLASTX
 NCBI GI g4322421
 BLAST score 250
 E value 2.0e-21
 Match length 66
 % identity 74
 NCBI Description (AF085230) cadmium resistance factor 1 [Arabidopsis thaliana]

Seq. No. 34402
 Seq. ID 2DA-01-Q1-B1-G2
 Method BLASTN
 NCBI GI g986968
 BLAST score 180
 E value 1.0e-96
 Match length 242
 % identity 94

Match length	129
% identity	66
NCBI Description	(AB009030) beta-Amyrin Synthase [Panax ginseng]
Seq. No.	34414
Seq. ID	2DC-02-Q1-B1-D10
Method	BLASTN
NCBI GI	g609224
BLAST score	156
E value	2.0e-82
Match length	296
% identity	88
NCBI Description	P.sativum mRNA for SAMS-2 >gi_609558_gb_L36681 PEADENSYNB Pisum sativum S-adenosylmethionine synthase mRNA, complete cds
Seq. No.	34415
Seq. ID	2DC-02-Q1-B1-D2
Method	BLASTX
NCBI GI	g1711618
BLAST score	375
E value	3.0e-36
Match length	107
% identity	68
NCBI Description	LOW AFFINITY SULPHATE TRANSPORTER 3 >gi_1085993_pir__S51765 low affinity sulphate transporter - Stylosanthes hamata >gi_607188_emb_CAA57831_(X82454) low affinity sulphate transporter [Stylosanthes hamata]
Seq. No.	34416
Seq. ID	2DC-02-Q1-B1-F11
Method	BLASTX
NCBI GI	g2832682
BLAST score	200
E value	1.0e-15
Match length	69
% identity	59
NCBI Description	(AL021712) hypothetical protein [Arabidopsis thaliana]
Seq. No.	34417
Seq. ID	2DC-02-Q1-B1-F4
Method	BLASTN
NCBI GI	g3790440
BLAST score	134
E value	3.0e-69
Match length	382
% identity	84
NCBI Description	Canavalia lineata chaperonin 60 alpha subunit mRNA, nuclear gene encoding chloroplast protein, complete cds
Seq. No.	34418
Seq. ID	2DC-02-Q1-B1-H12
Method	BLASTX
NCBI GI	g3355476
BLAST score	174
E value	1.0e-12
Match length	68

Method BLASTX
 NCBI GI g2781355
 BLAST score 306
 E value 5.0e-28
 Match length 122
 % identity 58
 NCBI Description (AC003113) F2401.11 [Arabidopsis thaliana]

Seq. No. 34425
 Seq. ID 6HA-01-Q1-B1-H1
 Method BLASTX
 NCBI GI g3914667
 BLAST score 235
 E value 1.0e-19
 Match length 94
 % identity 55
 NCBI Description 50S RIBOSOMAL PROTEIN L28, CHLOROPLAST PRECURSOR
 >gi_2459427 (AC002332) putative chloroplast 50S ribosomal
 protein L28 [Arabidopsis thaliana]

Seq. No. 34426
 Seq. ID 6HA-01-Q1-B1-H11
 Method BLASTX
 NCBI GI g2656003
 BLAST score 231
 E value 2.0e-19
 Match length 63
 % identity 68
 NCBI Description (Z98980) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 34427
 Seq. ID 6HA-01-Q1-E1-A9
 Method BLASTN
 NCBI GI g2588608
 BLAST score 189
 E value 1.0e-102
 Match length 193
 % identity 99
 NCBI Description Human BAC clone RG385F02 from 7p15, complete sequence [Homo sapiens]

Seq. No. 34428
 Seq. ID 6HA-01-Q1-E1-B9
 Method BLASTN
 NCBI GI g392590
 BLAST score 106
 E value 2.0e-52
 Match length 296
 % identity 95
 NCBI Description Human immunoglobulin heavy chain variable region (clone Amul4-3) mRNA, partial cds

Seq. No. 34429
 Seq. ID 6HA-01-Q1-E1-D12
 Method BLASTN
 NCBI GI g392865
 BLAST score 397

Seq. No. 34440
 Seq. ID 6HA-02-Q1-B1-A5
 Method BLASTX
 NCBI GI g1865677
 BLAST score 329
 E value 5.0e-31
 Match length 84
 % identity 76
 NCBI Description (Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No. 34441
 Seq. ID 6HA-02-Q1-B1-A6
 Method BLASTX
 NCBI GI g4038055
 BLAST score 172
 E value 2.0e-12
 Match length 102
 % identity 38
 NCBI Description (AC005897) putative cytochrome P450 [Arabidopsis thaliana]
 >gi_4557077_gb_AAD22516.1_AC007045_16 (AC007045) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No. 34442
 Seq. ID 6HA-02-Q1-B1-A8
 Method BLASTX
 NCBI GI g4455274
 BLAST score 438
 E value 2.0e-43
 Match length 111
 % identity 78
 NCBI Description (AL035527) spliceosome associated protein-like [Arabidopsis thaliana]

Seq. No. 34443
 Seq. ID 6HA-02-Q1-B1-B2
 Method BLASTX
 NCBI GI g2388577
 BLAST score 392
 E value 4.0e-38
 Match length 128
 % identity 60
 NCBI Description (AC000098) Similar to Arabidopsis putative ion-channel
 PID:g2262157 (gb_AC002329). [Arabidopsis thaliana]

Seq. No. 34444
 Seq. ID 6HA-02-Q1-B1-C11
 Method BLASTX
 NCBI GI g3242708
 BLAST score 141
 E value 1.0e-08
 Match length 90
 % identity 33
 NCBI Description (AC003040) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 34445
 Seq. ID 6HA-02-Q1-B1-D3
 Method BLASTX
 NCBI GI g3337367
 BLAST score 268
 E value 1.0e-23
 Match length 109
 % identity 48
 NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No. 34446
 Seq. ID 6HA-02-Q1-B1-D6
 Method BLASTX
 NCBI GI g3024021
 BLAST score 165
 E value 1.0e-14
 Match length 81
 % identity 57
 NCBI Description INITIATION FACTOR 5A-4 (EIF-5A) (EIF-4D)
 >gi_2225883_dbj_BAA20878_ (AB004825) eukaryotic initiation
 factor 5A4 [Solanum tuberosum]

Seq. No. 34447
 Seq. ID 6HA-02-Q1-B1-E2
 Method BLASTX
 NCBI GI g1657615
 BLAST score 381
 E value 8.0e-37
 Match length 87
 % identity 82
 NCBI Description (U72502) Glp [Arabidopsis thaliana] >gi_3068706 (AF049236)
 putative transmembrane protein Glp [Arabidopsis thaliana]

Seq. No. 34448
 Seq. ID 6HA-02-Q1-B1-F6
 Method BLASTX
 NCBI GI g3176686
 BLAST score 240
 E value 2.0e-20
 Match length 65
 % identity 71
 NCBI Description (AC003671) Similar to high affinity potassium transporter,
 HAK1 protein gb_U22945 from Schwanniomyces occidentalis.
 [Arabidopsis thaliana]

Seq. No. 34449
 Seq. ID 6HA-02-Q1-B1-G11
 Method BLASTX
 NCBI GI g2252843
 BLAST score 207
 E value 2.0e-16
 Match length 109
 % identity 48
 NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 34450
 Seq. ID 6HA-02-Q1-B1-H6

09634016-101000

Method BLASTX
 NCBI GI g99741
 BLAST score 268
 E value 1.0e-23
 Match length 91
 % identity 62
 NCBI Description P-glycoprotein pgp1 - Arabidopsis thaliana

Seq. No. 34451
 Seq. ID 6HA-02-Q1-E1-A5
 Method BLASTX
 NCBI GI g1865677
 BLAST score 187
 E value 4.0e-14
 Match length 49
 % identity 73
 NCBI Description (Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No. 34452
 Seq. ID 6HA-02-Q1-E1-B2
 Method BLASTX
 NCBI GI g2388577
 BLAST score 170
 E value 5.0e-12
 Match length 94
 % identity 46
 NCBI Description (AC000098) Similar to Arabidopsis putative ion-channel
 PID:g2262157 (gb_AC002329). [Arabidopsis thaliana]

Seq. No. 34453
 Seq. ID 6HA-02-Q1-E1-E1
 Method BLASTX
 NCBI GI g2465015
 BLAST score 180
 E value 3.0e-13
 Match length 97
 % identity 39
 NCBI Description (AJ001449) ripening-induced protein [Fragaria vesca]

Seq. No. 34454
 Seq. ID 6HA-02-Q1-E1-F1
 Method BLASTX
 NCBI GI g123554
 BLAST score 288
 E value 6.0e-26
 Match length 64
 % identity 86
 NCBI Description 18.1 KD CLASS I HEAT SHOCK PROTEIN >gi_99978_pir_S16248
 heat shock protein 18 (clone pMsHsp18.1) - alfalfa
 (fragment) >gi_19616_emb_CAA41546_ (X58710) heat shock
 protein [Medicago sativa]

Seq. No. 34455
 Seq. ID 6HA-02-Q1-E1-H6
 Method BLASTX
 NCBI GI g419760

BLAST score 43
 E value 2.0e-15
 Match length 87
 % identity 87
 NCBI Description Cloning vector pSport1, complete cds

Seq. No. 34497
 Seq. ID LIB3027-006-Q1-B1-E10
 Method BLASTN
 NCBI GI g736001
 BLAST score 155
 E value 7.0e-82
 Match length 243
 % identity 91
 NCBI Description G.soja (SH1) Gy5 mRNA for glycinin

Seq. No. 34498
 Seq. ID LIB3027-006-Q1-B1-E7
 Method BLASTN
 NCBI GI g18749
 BLAST score 144
 E value 2.0e-75
 Match length 202
 % identity 96
 NCBI Description G.max mRNA for seed maturation polypeptide

Seq. No. 34499
 Seq. ID LIB3027-006-Q1-B1-F9
 Method BLASTN
 NCBI GI g12974
 BLAST score 51
 E value 8.0e-20
 Match length 51
 % identity 100
 NCBI Description Soybean mitochondrial COII gene for cytochrome oxidase subunit II and tRNA-Met (CAT) gene (upstream)

Seq. No. 34500
 Seq. ID LIB3027-006-Q1-B1-H10
 Method BLASTN
 NCBI GI g18535
 BLAST score 76
 E value 7.0e-35
 Match length 88
 % identity 97
 NCBI Description Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No. 34501
 Seq. ID LIB3027-006-Q1-B1-H3
 Method BLASTN
 NCBI GI g56539
 BLAST score 33
 E value 4.0e-09
 Match length 152
 % identity 86
 NCBI Description R.norvegicus gene encoding prolactin, exon 5
 >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene

Seq. No. 34507
 Seq. ID LIB3027-008-Q1-B1-H7
 Method BLASTX
 NCBI GI g3413170
 BLAST score 171
 E value 3.0e-12
 Match length 101
 % identity 42
 NCBI Description (AJ010227) 40S ribosomal protein S6 [Cicer arietinum]

Seq. No. 34508
 Seq. ID LIB3027-010-Q1-B1-A1
 Method BLASTN
 NCBI GI g1794171
 BLAST score 101
 E value 1.0e-49
 Match length 289
 % identity 84
 NCBI Description Glycine max lipoxygenase-3 mRNA, complete cds

Seq. No. 34509
 Seq. ID LIB3027-010-Q1-B1-A6
 Method BLASTN
 NCBI GI g1389896
 BLAST score 32
 E value 1.0e-08
 Match length 184
 % identity 80
 NCBI Description Glycine max 68 kDa LEA protein mRNA, complete cds

Seq. No. 34510
 Seq. ID LIB3027-010-Q1-B1-E10
 Method BLASTX
 NCBI GI g3193306
 BLAST score 484
 E value 6.0e-49
 Match length 126
 % identity 79
 NCBI Description (AF069300) contains similarity to Arabidopsis membrane-associated salt-inducible-like protein (GB:AL021637) [Arabidopsis thaliana]

Seq. No. 34511
 Seq. ID LIB3027-010-Q1-B1-G3
 Method BLASTX
 NCBI GI g138364
 BLAST score 119
 E value 4.0e-15
 Match length 67
 % identity 53
 NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir_GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No. 34512

BLAST score 419
 E value 3.0e-41
 Match length 130
 % identity 58
 NCBI Description (AC004669) hypothetical protein [Arabidopsis thaliana]

Seq. No. 34523
 Seq. ID LIB3028-003-Q1-B1-C3
 Method BLASTX
 NCBI GI g4455169
 BLAST score 159
 E value 9.0e-11
 Match length 92
 % identity 39
 NCBI Description (AL035521) putative aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No. 34524
 Seq. ID LIB3028-003-Q1-B1-C5
 Method BLASTX
 NCBI GI g2160189
 BLAST score 353
 E value 1.0e-33
 Match length 126
 % identity 8
 NCBI Description (AC000132) Similar to A. thaliana receptor-like protein kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475, gb_ATTS4362 come from this gene. [Arabidopsis thaliana]

Seq. No. 34525
 Seq. ID LIB3028-003-Q1-B1-F2
 Method BLASTX
 NCBI GI g4467110
 BLAST score 599
 E value 2.0e-62
 Match length 124
 % identity 89
 NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 34526
 Seq. ID LIB3028-003-Q1-B1-G10
 Method BLASTN
 NCBI GI g2564336
 BLAST score 104
 E value 2.0e-51
 Match length 284
 % identity 84
 NCBI Description Brassica campestris mRNA for Tat binding protein 1, complete cds

Seq. No. 34527
 Seq. ID LIB3028-003-Q1-B1-G11
 Method BLASTN
 NCBI GI g609224
 BLAST score 186
 E value 1.0e-100
 Match length 318

% identity 90
 NCBI Description P.sativum mRNA for SAMS-2 >gi_609558_gb_L36681_PeADENSYNB
 Pisum sativum S-adenosylmethionine synthase mRNA, complete
 cds

Seq. No. 34528
 Seq. ID LIB3028-003-Q1-B1-G2
 Method BLASTX
 NCBI GI g3043529
 BLAST score 147
 E value 2.0e-09
 Match length 38
 % identity 66
 NCBI Description (AJ002204) polyamine oxidase [Zea mays]

Seq. No. 34529
 Seq. ID LIB3028-003-Q1-B1-H12
 Method BLASTN
 NCBI GI g2606080
 BLAST score 157
 E value 4.0e-83
 Match length 313
 % identity 88
 NCBI Description Glycine max sucrose synthase (SS) mRNA, complete cds

Seq. No. 34530
 Seq. ID LIB3028-004-Q1-B1-E11
 Method BLASTX
 NCBI GI g3135264
 BLAST score 353
 E value 2.0e-33
 Match length 89
 % identity 76
 NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]

Seq. No. 34531
 Seq. ID LIB3028-004-Q1-B1-H12
 Method BLASTN
 NCBI GI g516853
 BLAST score 254
 E value 1.0e-141
 Match length 346
 % identity 27
 NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds

Seq. No. 34532
 Seq. ID LIB3028-005-Q1-B1-B10
 Method BLASTX
 NCBI GI g1168196
 BLAST score 210
 E value 6.0e-17
 Match length 67
 % identity 67
 NCBI Description 14-3-3-LIKE PROTEIN >gi_555974 (U15036) 14-3-3-like protein
 [Pisum sativum]

Seq. No. 34533

Seq. ID LIB3028-006-Q1-B1-A10
 Method BLASTX
 NCBI GI g115797
 BLAST score 285
 E value 1.0e-25
 Match length 94
 % identity 57
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR
 (CAB-215) (LHCP) >gi_100026_pir_S16592 chlorophyll
 a/b-binding protein - garden pea >gi_20658_emb_CAA40365
 (X57082) chlorophyll a/b-binding protein [Pisum sativum]

Seq. No. 34539
 Seq. ID LIB3028-006-Q1-B1-A5
 Method BLASTN
 NCBI GI g1944318
 BLAST score 284
 E value 1.0e-158
 Match length 326
 % identity 99
 NCBI Description Glycine max mRNA for cysteine proteinase inhibitor,
 complete cds

Seq. No. 34540
 Seq. ID LIB3028-006-Q1-B1-C5
 Method BLASTX
 NCBI GI g1350720
 BLAST score 216
 E value 1.0e-17
 Match length 91
 % identity 50
 NCBI Description 60S RIBOSOMAL PROTEIN L32

Seq. No. 34541
 Seq. ID LIB3028-006-Q1-B1-E12
 Method BLASTX
 NCBI GI g1669341
 BLAST score 262
 E value 8.0e-23
 Match length 118
 % identity 47
 NCBI Description (D45066) AOBP (ascorbate oxidase promoter-binding protein)
 [Cucurbita maxima]

Seq. No. 34542
 Seq. ID LIB3028-006-Q1-B1-E7
 Method BLASTX
 NCBI GI g3176098
 BLAST score 341
 E value 3.0e-32
 Match length 107
 % identity 67
 NCBI Description (Y15036) annexin [Medicago truncatula]

Seq. No. 34543
 Seq. ID LIB3028-006-Q1-B1-G7
 Method BLASTX

00684016-10000

NCBI GI g3128218
BLAST score 395
E value 2.0e-38
Match length 119
% identity 66
NCBI Description (AC004077) putative end13 protein [Arabidopsis thaliana]

Seq. No. 34544
Seq. ID LIB3028-006-Q1-B1-H1
Method BLASTX
NCBI GI g123650
BLAST score 301
E value 1.0e-27
Match length 109
% identity 58
NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN >gi_82245_pir_S03250 heat shock protein 70 (clone pMON9743) - garden petunia
>gi_20557_emb_CAA30018_ (X06932) heat shock protein 70 [Petunia x hybrida]

Seq. No. 34545
Seq. ID LIB3028-007-Q1-B1-A4
Method BLASTX
NCBI GI g3738299
BLAST score 363
E value 1.0e-34
Match length 101
% identity 72
NCBI Description (AC005309) putative glutaredoxin [Arabidopsis thaliana]
>gi_4249395 (AC006072) putative glutaredoxin [Arabidopsis thaliana]

Seq. No. 34546
Seq. ID LIB3028-007-Q1-B1-A9
Method BLASTN
NCBI GI g2935449
BLAST score 73
E value 6.0e-33
Match length 109
% identity 92
NCBI Description Malus domestica histone H2B mRNA, partial cds

Seq. No. 34547
Seq. ID LIB3028-007-Q1-B1-B8
Method BLASTX
NCBI GI g4558673
BLAST score 244
E value 9.0e-21
Match length 125
% identity 33
NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No. 34548
Seq. ID LIB3028-007-Q1-B1-C7
Method BLASTN
NCBI GI g2760168
BLAST score 44

E value 1.0e-15
 Match length 215
 % identity 81
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No. 34549
 Seq. ID LIB3028-007-Q1-B1-D10
 Method BLASTX
 NCBI GI g2894606
 BLAST score 208
 E value 2.0e-16
 Match length 76
 % identity 55
 NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 34550
 Seq. ID LIB3028-007-Q1-B1-E7
 Method BLASTX
 NCBI GI g267079
 BLAST score 505
 E value 2.0e-51
 Match length 131
 % identity 75
 NCBI Description TUBULIN BETA-6 CHAIN >gi_320187_pir_JQ1590 tubulin beta-6 chain - Arabidopsis thaliana >gi_166904 (M84703) beta-6 tubulin [Arabidopsis thaliana]

Seq. No. 34551
 Seq. ID LIB3028-007-Q1-B1-H4
 Method BLASTN
 NCBI GI g18551
 BLAST score 289
 E value 1.0e-162
 Match length 364
 % identity 95
 NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding protein

Seq. No. 34552
 Seq. ID LIB3028-008-Q1-B1-A10
 Method BLASTX
 NCBI GI g3608479
 BLAST score 240
 E value 2.0e-20
 Match length 60
 % identity 78
 NCBI Description (AF088912)-ribosomal protein L15 [Petunia x hybrida]

Seq. No. 34553
 Seq. ID LIB3028-008-Q1-B1-B2
 Method BLASTX
 NCBI GI g1488255
 BLAST score 172
 E value 2.0e-12
 Match length 59
 % identity 49

NCBI Description (U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]
 >gi_2961381_emb_CAA18128_(AL022141) ferulate-5-hydroxylase
 (FAH1) [Arabidopsis thaliana] >gi_3925365 (AF068574)
 ferulate-5-hydroxylase [Arabidopsis thaliana]

Seq. No. 34554
 Seq. ID LIB3028-008-Q1-B1-F2
 Method BLASTX
 NCBI GI g2642154
 BLAST score 162
 E value 8.0e-14
 Match length 91
 % identity 55

NCBI Description (AC003000) unknown protein [Arabidopsis thaliana]
 >gi_3790595 (AF079186) RING-H2 finger protein RHC2a
 [Arabidopsis thaliana]

Seq. No. 34555
 Seq. ID LIB3028-008-Q1-B1-G7
 Method BLASTN
 NCBI GI g312988
 BLAST score 130
 E value 6.0e-67
 Match length 258
 % identity 88
 NCBI Description G.max mRNA for beta-tubulin, partial cds

Seq. No. 34556
 Seq. ID LIB3028-009-Q1-B1-A6
 Method BLASTX
 NCBI GI g549986
 BLAST score 541
 E value 2.0e-55
 Match length 141
 % identity 75
 NCBI Description (U13149) possible apospory-associated protein [Pennisetum
 ciliare]

Seq. No. 34557
 Seq. ID LIB3028-009-Q1-B1-B1
 Method BLASTN
 NCBI GI g303900
 BLAST score 209
 E value 1.0e-114
 Match length 293
 % identity 28
 NCBI Description Soybean gene for ubiquitin, complete cds

Seq. No. 34558
 Seq. ID LIB3028-009-Q1-B1-C12
 Method BLASTX
 NCBI GI g3522929
 BLAST score 339
 E value 6.0e-32
 Match length 78
 % identity 82
 NCBI Description (AC002535) putative dTDP-glucose 4-6-dehydratase

NCBI GI g170087
 BLAST score 91
 E value 7.0e-44
 Match length 171
 % identity 88
 NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)

Seq. No. 34570
 Seq. ID LIB3028-011-Q1-B1-E8
 Method BLASTN
 NCBI GI g310575
 BLAST score 254
 E value 1.0e-141
 Match length 413
 % identity 93
 NCBI Description Glycine max nodulin-26 mRNA, complete cds

Seq. No. 34571
 Seq. ID LIB3028-011-Q1-B1-F1
 Method BLASTX
 NCBI GI g3176715
 BLAST score 381
 E value 8.0e-37
 Match length 117
 % identity 64
 NCBI Description (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 34572
 Seq. ID LIB3028-011-Q1-B1-G8
 Method BLASTX
 NCBI GI g2088643
 BLAST score 237
 E value 4.0e-20
 Match length 64
 % identity 36
 NCBI Description (AF002109) transcription factor SF3 isolog [Arabidopsis thaliana]

Seq. No. 34573
 Seq. ID LIB3028-011-Q1-B1-H2
 Method BLASTN
 NCBI GI g1408470
 BLAST score 38
 E value 3.0e-12
 Match length 110
 % identity 84
 NCBI Description Arabidopsis thaliana actin depolymerizing factor 1 (AtADF1) mRNA, complete cds

Seq. No. 34574
 Seq. ID LIB3028-012-Q1-B1-C11
 Method BLASTX
 NCBI GI g4539333
 BLAST score 345
 E value 1.0e-32
 Match length 110

% identity	61
NCBI Description	(AL035539) putative amino acid transport protein [Arabidopsis thaliana]
Seq. No.	34575
Seq. ID	LIB3028-012-Q1-B1-G12
Method	BLASTX
NCBI GI	g1171642
BLAST score	216
E value	2.0e-17
Match length	90
% identity	50
NCBI Description	PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK >gi_481206_pir_S38326 protein kinase - Arabidopsis thaliana >gi_166809 (L07248) protein kinase [Arabidopsis thaliana]
Seq. No.	34576
Seq. ID	LIB3028-013-Q1-B1-A11
Method	BLASTX
NCBI GI	g2129889
BLAST score	269
E value	5.0e-31
Match length	95
% identity	76
NCBI Description	methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea
Seq. No.	34577
Seq. ID	LIB3028-013-Q1-B1-C4
Method	BLASTX
NCBI GI	g2505884
BLAST score	282
E value	3.0e-25
Match length	90
% identity	59
NCBI Description	(Y12776) hypothetical protein [Arabidopsis thaliana]
Seq. No.	34578
Seq. ID	LIB3028-013-Q1-B1-E1
Method	BLASTX
NCBI GI	g951449
BLAST score	214
E value	6.0e-25
Match length	96
% identity	59
NCBI Description	(L46681) aspartic protease precursor [Lycopersicon esculentum]
Seq. No.	34579
Seq. ID	LIB3028-013-Q1-B1-F1
Method	BLASTN
NCBI GI	g2463568
BLAST score	48
E value	3.0e-18
Match length	173
% identity	81
NCBI Description	Glycine max mRNA for squalene synthase, complete cds

Seq. No. 34585
 Seq. ID LIB3028-014-Q1-B1-D1
 Method BLASTN
 NCBI GI g2570122
 BLAST score 33
 E value 5.0e-09
 Match length 41
 % identity 95
 NCBI Description S.latifolia mRNA, clone CCLS 30.1-21

Seq. No. 34586
 Seq. ID LIB3028-014-Q1-B1-E9
 Method BLASTX
 NCBI GI g4572673
 BLAST score 297
 E value 5.0e-27
 Match length 103
 % identity 54
 NCBI Description (AC006954) putative sarcosine oxidase [Arabidopsis thaliana]

Seq. No. 34587
 Seq. ID LIB3028-014-Q1-B1-G4
 Method BLASTX
 NCBI GI g1515454
 BLAST score 147
 E value 1.0e-09
 Match length 69
 % identity 46
 NCBI Description (U64448) lac repressor [Cloning vector pCMVLacI]

Seq. No. 34588
 Seq. ID LIB3028-015-Q1-B1-A11
 Method BLASTX
 NCBI GI g267124
 BLAST score 184
 E value 4.0e-23
 Match length 96
 % identity 61
 NCBI Description THIOREDOXIN H-TYPE 1 (TRX-H1) >gi_100387_pir_S16590
 thioredoxin h1 - common tobacco >gi_20047_emb_CAA41415_
 (X58527) thioredoxin [Nicotiana tabacum]

Seq. No. 34589
 Seq. ID LIB3028-015-Q1-B1-C5
 Method BLASTX
 NCBI GI g1172664
 BLAST score 383
 E value 4.0e-37
 Match length 118
 % identity 66
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
 (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
 >gi_419791_pir_S31165 photosystem I chain III precursor -
 Flaveria trinervia >gi_298482_bbs_127083 photosystem I
 reaction center subunit III, PSI-RC PsaF [Flaveria

BLAST score 300
 E value 1.0e-27
 Match length 84
 % identity 67
 NCBI Description (U90439) phospholipase D isolog [Arabidopsis thaliana]

Seq. No. 34601
 Seq. ID LIB3028-018-Q1-B1-B1
 Method BLASTN
 NCBI GI g3021484
 BLAST score 36
 E value 7.0e-11
 Match length 68
 % identity 88
 NCBI Description Lycopersicon esculentum H2B-3 mRNA for histone H2B

Seq. No. 34602
 Seq. ID LIB3028-018-Q1-B1-C2
 Method BLASTX
 NCBI GI g2129879
 BLAST score 190
 E value 1.0e-17
 Match length 108
 % identity 50
 NCBI Description chlorophyll a/b-binding protein type II precursor,
 photosystem I - garden pea >gi_602359_emb_CAA57492
 (X81962) Type II chlorophyll a/b binding protein from
 photosystem I [Pisum sativum]

Seq. No. 34603
 Seq. ID LIB3028-018-Q1-B1-C5
 Method BLASTN
 NCBI GI g2764803
 BLAST score 122
 E value 4.0e-62
 Match length 310
 % identity 85
 NCBI Description G.max mRNA for epoxide hydrolase

Seq. No. 34604
 Seq. ID LIB3028-018-Q1-B1-D6
 Method BLASTX
 NCBI GI g2618705
 BLAST score 257
 E value 2.0e-26
 Match length 93
 % identity 43
 NCBI Description (AC002510) putative ABC transporter, 5' partial
 [Arabidopsis thaliana]

Seq. No. 34605
 Seq. ID LIB3028-018-Q1-B1-E9
 Method BLASTX
 NCBI GI g4455276
 BLAST score 393
 E value 3.0e-38
 Match length 123

Seq. No. 34611
 Seq. ID LIB3028-019-Q1-B1-A12
 Method BLASTX
 NCBI GI g2708331
 BLAST score 286
 E value 1.0e-25
 Match length 94
 % identity 61
 NCBI Description (AF038557) ligand gated channel-like protein [Arabidopsis thaliana]

Seq. No. 34612
 Seq. ID LIB3028-019-Q1-B1-A7
 Method BLASTN
 NCBI GI g1256365
 BLAST score 41
 E value 6.0e-14
 Match length 65
 % identity 91
 NCBI Description Promoter-trapping vector pdeltagusBin19

Seq. No. 34613
 Seq. ID LIB3028-019-Q1-B1-B11
 Method BLASTX
 NCBI GI g2832640
 BLAST score 347
 E value 6.0e-33
 Match length 105
 % identity 65
 NCBI Description (AL021710) neoxanthin cleavage enzyme - like protein [Arabidopsis thaliana]

Seq. No. 34614
 Seq. ID LIB3028-019-Q1-B1-B6
 Method BLASTX
 NCBI GI g309673
 BLAST score 213
 E value 2.0e-17
 Match length 81
 % identity 62
 NCBI Description (L19651) light harvesting protein [Pisum sativum]

Seq. No. 34615
 Seq. ID LIB3028-019-Q1-B1-B7
 Method BLASTN
 NCBI GI g1399379
 BLAST score 106
 E value 9.0e-53
 Match length 122
 % identity 97
 NCBI Description Glycine max S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase mRNA, complete cds

Seq. No. 34616
 Seq. ID LIB3028-019-Q1-B1-C5
 Method BLASTX

NCBI GI g542005
 BLAST score 181
 E value 1.0e-13
 Match length 71
 % identity 56
 NCBI Description endoxyloglucan transferase - adzuki bean
 >gi_469510_dbj_BAA03925_ (D16458) endo-xyloglucan
 transferase [Vigna angularis]

Seq. No. 34617
 Seq. ID LIB3028-019-Q1-B1-C6
 Method BLASTN
 NCBI GI g18551
 BLAST score 132
 E value 3.0e-68
 Match length 236
 % identity 89
 NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
 protein

Seq. No. 34618
 Seq. ID LIB3028-019-Q1-B1-D1
 Method BLASTX
 NCBI GI g1346701
 BLAST score 284
 E value 2.0e-25
 Match length 110
 % identity 48
 NCBI Description EXOPOLYGALACTURONASE CLONE GBGE184 PRECURSOR (EXOPG)
 (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
 >gi_421831_pir_S34199 exopolygalacturonase (clone GBGe184)
 - Arabidopsis thaliana >gi_313682_emb_CAA51032_ (X72291)
 exopolygalacturonase [Arabidopsis thaliana]
 >gi_3004440_emb_CAA76127_ (Y16230) polygalacturonase
 [Arabidopsis thaliana]

Seq. No. 34619
 Seq. ID LIB3028-019-Q1-B1-E11
 Method BLASTX
 NCBI GI g4100433
 BLAST score 234
 E value 1.0e-19
 Match length 50
 % identity 82
 NCBI Description (AF000378) beta-glucosidase [Glycine max]

Seq. No. 34620
 Seq. ID LIB3028-019-Q1-B1-F5
 Method BLASTN
 NCBI GI g18557
 BLAST score 84
 E value 1.0e-39
 Match length 136
 % identity 91
 NCBI Description G.max mRNA for ACC synthase

Seq. No. 34621

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Seq. No.      34626
Seq. ID      LIB3028-020-Q1-B1-E3
Method       BLASTX
NCBI GI      g1408296
BLAST score   176
E value      3.0e-13
```


Seq. ID LIB3028-023-Q1-B1-C5
 Method BLASTX
 NCBI GI g2104536
 BLAST score 141
 E value 1.0e-08
 Match length 56
 % identity 59
 NCBI Description (AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

Seq. No. 34644
 Seq. ID LIB3028-024-Q1-B1-A6
 Method BLASTN
 NCBI GI g2182285
 BLAST score 57
 E value 3.0e-23
 Match length 125
 % identity 86
 NCBI Description Sequence of BAC F5I14 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 34645
 Seq. ID LIB3028-024-Q1-B1-C3
 Method BLASTX
 NCBI GI g4522012
 BLAST score 158
 E value 1.0e-10
 Match length 93
 % identity 41
 NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 34646
 Seq. ID LIB3028-024-Q1-B1-E11
 Method BLASTX
 NCBI GI g4006827
 BLAST score 313
 E value 7.0e-29
 Match length 115
 % identity 55
 NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 34647
 Seq. ID LIB3028-024-Q1-B1-F2
 Method BLASTX
 NCBI GI g3152613
 BLAST score 280
 E value 5.0e-25
 Match length 113
 % identity 52
 NCBI Description (AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No. 34648
 Seq. ID LIB3028-024-Q1-B1-H4
 Method BLASTX
 NCBI GI g2828280
 BLAST score 192
 E value 7.0e-15

0954015-101000

Match length	47
% identity	74
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana] >gi_2832633_emb_CAA16762_ (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.	34649
Seq. ID	LIB3028-024-Q1-B1-H8
Method	BLASTX
NCBI GI	g3402684
BLAST score	150
E value	7.0e-10
Match length	40
% identity	72
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]
Seq. No.	34650
Seq. ID	LIB3028-025-Q1-B1-B10
Method	BLASTX
NCBI GI	g1345785
BLAST score	536
E value	1.0e-56
Match length	126
% identity	94
NCBI Description	CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE 1) >gi_567935_dbj_BAA05640_ (D26593) chalcone synthase [Camellia sinensis]
Seq. No.	34651
Seq. ID	LIB3028-025-Q1-B1-F1
Method	BLASTX
NCBI GI	g2982431
BLAST score	203
E value	6.0e-16
Match length	125
% identity	3
NCBI Description	(AL022224) leucine rich repeat-like protein [Arabidopsis thaliana]
Seq. No.	34652
Seq. ID	LIB3028-026-Q1-B1-A4
Method	BLASTX
NCBI GI	g3176874
BLAST score	179
E value	4.0e-13
Match length	45
% identity	69
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]
Seq. No.	34653
Seq. ID	LIB3028-026-Q1-B1-F12
Method	BLASTX
NCBI GI	g4468993
BLAST score	543
E value	8.0e-56
Match length	123

Match length 84
% identity 33
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 34690
Seq. ID LIB3028-034-Q1-B1-F12
Method BLASTN
NCBI GI g516853
BLAST score 181
E value 2.0e-97
Match length 317
% identity 38
NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds

Seq. No. 34691
Seq. ID LIB3028-034-Q1-B1-H1
Method BLASTX
NCBI GI g3435096
BLAST score 381
E value 9.0e-37
Match length 98
% identity 73
NCBI Description (AF033587) SRZ-80 [Arabidopsis thaliana]

Seq. No. 34692
Seq. ID LIB3028-034-Q1-B1-H2
Method BLASTX
NCBI GI g1345132
BLAST score 323
E value 4.0e-30
Match length 108
% identity 62
NCBI Description (U47029) ERECTA [Arabidopsis thaliana]
>gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase
[Arabidopsis thaliana] >gi_3075386 (AC004484) receptor
protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No. 34693
Seq. ID LIB3028-035-Q1-B1-A4
Method BLASTX
NCBI GI g3063448
BLAST score 290
E value 4.0e-26
Match length 126
% identity 47
NCBI Description (AC003981) F22013.10 [Arabidopsis thaliana]

Seq. No. 34694
Seq. ID LIB3028-035-Q1-B1-B2
Method BLASTX
NCBI GI g3776005
BLAST score 222
E value 3.0e-18
Match length 48
% identity 94
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. ID LIB3028-040-Q1-B1-D11
 Method BLASTX
 NCBI GI g1871192
 BLAST score 589
 E value 3.0e-61
 Match length 112
 % identity 87
 NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No. 34723
 Seq. ID LIB3028-041-Q1-B1-A12
 Method BLASTX
 NCBI GI g1297189
 BLAST score 329
 E value 8.0e-31
 Match length 107
 % identity 62
 NCBI Description (U53501) Theoretical protein with similarity to Swiss-Prot Accession Number P19456 plasma membrane ATPase 2 (proton pump) [Arabidopsis thaliana]

Seq. No. 34724
 Seq. ID LIB3028-041-Q1-B1-A8
 Method BLASTN
 NCBI GI g516853
 BLAST score 134
 E value 3.0e-69
 Match length 287
 % identity 45
 NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds

Seq. No. 34725
 Seq. ID LIB3028-041-Q1-B1-B2
 Method BLASTX
 NCBI GI g541943
 BLAST score 273
 E value 3.0e-24
 Match length 55
 % identity 85
 NCBI Description metallothionein - soybean >gi_228682_prf_1808316A metallothionein-like protein [Glycine max]

Seq. No. 34726
 Seq. ID LIB3028-041-Q1-B1-E12
 Method BLASTX
 NCBI GI g3281853
 BLAST score 141
 E value 5.0e-09
 Match length 44
 % identity 68
 NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 34727
 Seq. ID LIB3028-041-Q1-B1-E8
 Method BLASTX
 NCBI GI g1568637

E value 6.0e-18
 Match length 48
 % identity 100
 NCBI Description Plumbago auriculata large subunit 26S ribosomal RNA gene, partial sequence

Seq. No. 34749
 Seq. ID LIB3028-046-Q1-B1-C9
 Method BLASTX
 NCBI GI g4007792
 BLAST score 283
 E value 2.0e-25
 Match length 96
 % identity 62
 NCBI Description (AL034463) Xenopus 14s cohesin smc1 subunit homolog [Schizosaccharomyces pombe]

Seq. No. 34750
 Seq. ID LIB3028-046-Q1-B1-D9
 Method BLASTX
 NCBI GI g4056433
 BLAST score 142
 E value 6.0e-09
 Match length 95
 % identity 40
 NCBI Description (AC005990) Similar to anter-specific proline-rich protein (CEX) gb_X60376 from Brassica napus. [Arabidopsis thaliana]

Seq. No. 34751
 Seq. ID LIB3028-046-Q1-B1-H1
 Method BLASTX
 NCBI GI g4210948
 BLAST score 127
 E value 2.0e-09
 Match length 77
 % identity 56
 NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No. 34752
 Seq. ID LIB3028-046-Q1-B1-H7
 Method BLASTX
 NCBI GI g3885329
 BLAST score 333
 E value 3.0e-31
 Match length 83
 % identity 78
 NCBI Description (AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No. 34753
 Seq. ID LIB3028-047-Q1-B1-H12
 Method BLASTX
 NCBI GI g2244899
 BLAST score 164
 E value 1.0e-11
 Match length 92
 % identity 43
 NCBI Description (Z97338) similar to UFD1 protein [Arabidopsis thaliana]

03684010

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Seq. No.      34760
Seq. ID      LIB3028-050-Q1-B1-H1
Method       BLASTX
NCBI GI      g3935183
BLAST score   174
E value      5.0e-13
Match length  75
% identity    52
NCBI Description (AC004557) F17L21.26 [Arabidopsis thaliana]
```

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Seq. No.          34761
Seq. ID           LIB3028-050-Q1-B1-H10
Method            BLASTX
NCBI GI           g3551247
BLAST score       331
E value           6.0e-31
Match length      75
% identity        77
NCBI Description   (AB012703) 181 [Daucus carota]
```

```
Seq. No.          34762
Seq. ID           LIB3028-050-Q1-B1-H5
Method            BLASTN
NCBI GI           g624937
BLAST score       40
E value           3.0e-13
Match length      104
% identity         86
NCBI Description  A.thaliana RPL16A gene
```

Seq. No.	34763
Seq. ID	LIB3028-051-Q1-B1-C12
Method	BLASTX
NCBI GI	g2827992
BLAST score	174
E value	9.0e-13
Match length	75
% identity	47
NCBI Description	(AF034743) UDP-glucuronosyltransferase [Pisum sativum]

5245

[illegible]

0-9

[illegible]

0-9

0-9

NCBI Description (AL035527) peptide transporter-like protein [Arabidopsis thaliana]

Seq. No. 34785
Seq. ID LIB3028-054-Q1-B1-D5
Method BLASTX
NCBI GI g2341032
BLAST score 210
E value 3.0e-17
Match length 47
% identity 83
NCBI Description (AC000104) EST gb_ATTS0956 comes from this gene.
[Arabidopsis thaliana]

Seq. No. 34786
Seq. ID LIB3028-054-Q1-B1-H11
Method BLASTX
NCBI GI g3269285
BLAST score 360
E value 2.0e-34
Match length 106
% identity 63
NCBI Description (AL030978) hypothetical protein [Arabidopsis thaliana]

Seq. No. 34787
Seq. ID LIB3028-054-Q1-B1-H3
Method BLASTX
NCBI GI g1346118
BLAST score 384
E value 3.0e-37
Match length 107
% identity 69
NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
>gi_542101_pir_S40215 H-protein - Flaveria pringlei
>gi_2119599_pir_S60194 H-protein precursor (clone HFP4) -
Flaveria pringlei >gi_438001_emb_CAA81075_(Z25856)
H-protein [Flaveria pringlei] >gi_3688301_emb_CAB16913_
(Z99764) H-protein [Flaveria pringlei]

Seq. No. 34788
Seq. ID LIB3028-054-Q1-B1-H8
Method BLASTX
NCBI GI g4309758
BLAST score 148
E value 2.0e-09
Match length 37
% identity 78
NCBI Description (AC006217) hypothetical protein [Arabidopsis thaliana]

Seq. No. 34789
Seq. ID LIB3028-055-Q1-B1-G5
Method BLASTN
NCBI GI g1055367
BLAST score 191
E value 1.0e-103
Match length 311
% identity 91

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No. 34790
Seq. ID LIB3028-056-Q1-B1-D2
Method BLASTX
NCBI GI g3114573
BLAST score 546
E value 4.0e-56
Match length 130
% identity 78
NCBI Description (AF019383) 1-deoxyxylulose-5-phosphate synthase [Mentha x piperita]

Seq. No. 34791
Seq. ID LIB3028-056-Q1-B1-D9
Method BLASTN
NCBI GI g1370171
BLAST score 47
E value 2.0e-17
Match length 59
% identity 95
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB1X

Seq. No. 34792
Seq. ID LIB3028-056-Q1-B1-F8
Method BLASTN
NCBI GI g56539
BLAST score 40
E value 4.0e-13
Match length 100
% identity 85
NCBI Description R.norvegicus gene encoding prolactin, exon 5
>gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
: exon v and flanks

Seq. No. 34793
Seq. ID LIB3028-056-Q1-B1-G10
Method BLASTX
NCBI GI g3860247
BLAST score 371
E value 1.0e-35
Match length 72
% identity 96
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 34794
Seq. ID LIB3028-056-Q1-B1-H12
Method BLASTX
NCBI GI g4559330
BLAST score 240
E value 2.0e-20
Match length 89
% identity 57
NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 34795

Seq. ID LIB3029-001-Q1-B1-B4
 Method BLASTX
 NCBI GI g731651
 BLAST score 308
 E value 3.0e-28
 Match length 124
 % identity 46
 NCBI Description HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN IN
 PUT2-SRB2 INTERGENIC REGION >gi_626608_pir_S46746
 hypothetical protein YHR039c - yeast (*Saccharomyces*
cerevisiae) >gi_488180 (U00062) Yhr039cp [*Saccharomyces*
cerevisiae]

Seq. No. 34796
 Seq. ID LIB3029-001-Q1-B1-C1
 Method BLASTX
 NCBI GI g2244852
 BLAST score 308
 E value 3.0e-28
 Match length 66
 % identity 85
 NCBI Description (Z97337) hypothetical protein [*Arabidopsis thaliana*]

Seq. No. 34797
 Seq. ID LIB3029-002-Q1-B1-A4
 Method BLASTN
 NCBI GI g1431744
 BLAST score 79
 E value 8.0e-37
 Match length 151
 % identity 88
 NCBI Description Glycine max sucrose binding protein (sbp) mRNA, complete
 cds

Seq. No. 34798
 Seq. ID LIB3029-002-Q1-B1-C3
 Method BLASTN
 NCBI GI g18540
 BLAST score 139
 E value 2.0e-72
 Match length 285
 % identity 87
 NCBI Description G.max BBI mRNA for proteinase inhibitor

Seq. No. 34799
 Seq. ID LIB3029-002-Q1-B1-D12
 Method BLASTX
 NCBI GI g1352345
 BLAST score 161
 E value 3.0e-15
 Match length 90
 % identity 58
 NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
 >gi_18765_emb_CAA40182_ (X56856) eEF-1a [*Glycine max*]

Seq. No. 34800
 Seq. ID LIB3029-002-Q1-B1-E3

NCBI Description (AC006403) hypothetical protein [Arabidopsis thaliana]
 Seq. No. 34827
 Seq. ID LIB3029-008-Q1-B1-C7
 Method BLASTX
 NCBI GI g2388937
 BLAST score 204
 E value 3.0e-16
 Match length 72
 % identity 50
 NCBI Description (Z98977) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 34828
 Seq. ID LIB3029-008-Q1-B1-H6
 Method BLASTX
 NCBI GI g3913952
 BLAST score 350
 E value 3.0e-33
 Match length 85
 % identity 73
 NCBI Description ADENYLATE KINASE (ATP-AMP TRANSPHOSPHORYLASE) >gi_2351578
 (U82330) adenylate kinase homolog [Prunus armeniaca]

Seq. No. 34829
 Seq. ID LIB3029-008-Q1-B1-H7
 Method BLASTX
 NCBI GI g3377507
 BLAST score 462
 E value 2.0e-46
 Match length 125
 % identity 69
 NCBI Description (AF056026) auxin transport protein EIR1 [Arabidopsis thaliana] >gi_3661620 (AF093241) putative auxin efflux carrier AGR [Arabidopsis thaliana] >gi_3746886 (AF087459) polar-auxin-transport efflux component AGRVITROPIC 1 [Arabidopsis thaliana] >gi_4206709 (AF086906) root gravitropism control protein [Arabidopsis thaliana]

Seq. No. 34830
 Seq. ID LIB3029-009-Q1-B1-A7
 Method BLASTN
 NCBI GI g18535
 BLAST score 299
 E value 1.0e-167
 Match length 365
 % identity 91
 NCBI Description Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No. 34831
 Seq. ID LIB3029-009-Q1-B1-B6
 Method BLASTX
 NCBI GI g3549626
 BLAST score 180
 E value 8.0e-14
 Match length 58
 % identity 53
 NCBI Description (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

Seq. No. 34832
Seq. ID LIB3029-009-Q1-B1-E5
Method BLASTX
NCBI GI g4097880
BLAST score 351
E value 2.0e-33
Match length 99
% identity 71
NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 34833
Seq. ID LIB3029-009-Q1-B1-G3
Method BLASTN
NCBI GI g3097320
BLAST score 190
E value 1.0e-102
Match length 265
% identity 95
NCBI Description Glycine max gene for Bd 30K, complete cds

Seq. No. 34834
Seq. ID LIB3029-009-Q1-B1-H8
Method BLASTN
NCBI GI g210811
BLAST score 110
E value 5.0e-55
Match length 253
% identity 88
NCBI Description Bean pod mottle virus coat protein gene, complete cds,
complete middle component (M) RNA

Seq. No. 34835
Seq. ID LIB3029-010-Q1-B1-A1
Method BLASTX
NCBI GI g2213594
BLAST score 221
E value 4.0e-18
Match length 73
% identity 60
NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No. 34836
Seq. ID LIB3029-010-Q1-B1-B3
Method BLASTN
NCBI GI g2905771
BLAST score 144
E value 3.0e-75
Match length 156
% identity 98
NCBI Description Glycine max glyceraldehyde-3 phosphate dehydrogenase
(GAPDH) mRNA, partial cds

Seq. No. 34837
Seq. ID LIB3029-010-Q1-B1-C10
Method BLASTN
NCBI GI g210811

Method	BLASTX
NCBI GI	g1931651
BLAST score	394
E value	2.0e-38
Match length	125
% identity	62
NCBI Description	(U95973) membrane-associated salt-inducible protein isolog [Arabidopsis thaliana]

Seq. No.	34854
Seq. ID	LIB3029-012-Q1-B1-G9
Method	BLASTX
NCBI GI	g229707
BLAST score	551
E value	8.0e-57
Match length	109
% identity	91
NCBI Description	Bean pod mottle virus

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Seq. No.      34855
Seq. ID      LIB3030-001-Q1-B1-D11
Method       BLASTX
NCBI GI      g2262105
BLAST score   199
E value      8.0e-16
Match length  81
% identity    41
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
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Seq. No.          34856
Seq. ID           LIB3030-001-Q1-B1-G6
Method            BLASTX
NCBI GI           g2160189
BLAST score       296
E value           8.0e-27
Match length      127
% identity        49
NCBI Description   (AC000132) Similar to A. thaliana receptor-like protein
                  kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come
                  from this gene. [Arabidopsis thaliana]
```

```
Seq. No.      34857
Seq. ID       LIB3030-001-Q1-B1-H12
Method        BLASTX
NCBI GI       g3378650
BLAST score   159
E value       3.0e-17
Match length  83
% identity    61
NCBI Description (X97606) abscisic acid activated [Medicago sativa]
```

```
Seq. No.      34858
Seq. ID       LIB3030-002-Q1-B1-A3
Method        BLASTX
NCBI GI       g3461829
BLAST score    179
E value       3.0e-13
```


NCBI Description (AL022580) cytochrome P450 [Arabidopsis thaliana]
Seq. No. 34875
Seq. ID LIB3030-005-Q1-B1-C1
Method BLASTX
NCBI GI g3252854
BLAST score 205
E value 1.0e-16
Match length 57
% identity 75
NCBI Description (AF020424) glutamate decarboxylase isozyme 2 [Nicotiana tabacum]

Seq. No. 34876
Seq. ID LIB3030-005-Q1-B1-C7
Method BLASTX
NCBI GI g3702368
BLAST score 214
E value 3.0e-17
Match length 69
% identity 59
NCBI Description (AJ001855) alpha subunit of F-actin capping protein [Arabidopsis thaliana]

Seq. No. 34877
Seq. ID LIB3030-005-Q1-B1-D5
Method BLASTN
NCBI GI g975703
BLAST score 40
E value 4.0e-13
Match length 119
% identity 50
NCBI Description P.sativum GR gene

Seq. No. 34878
Seq. ID LIB3030-005-Q1-B1-D6
Method BLASTX
NCBI GI g2073450
BLAST score 428
E value 3.0e-42
Match length 93
% identity 85
NCBI Description (Y12859) Krm protein [Lotus japonicus]

Seq. No. 34879
Seq. ID LIB3030-005-Q1-B1-D8
Method BLASTX
NCBI GI g4204695
BLAST score 179
E value 4.0e-13
Match length 93
% identity 41
NCBI Description (AF117062) putative inositol polyphosphate 5-phosphatase At5P1 [Arabidopsis thaliana]

Seq. No. 34880
Seq. ID LIB3030-005-Q1-B1-E12

Match length 54
% identity 69
NCBI Description (AB003131) endonuclease [Zinnia elegans]

Seq. No. 34886
Seq. ID LIB3030-007-Q1-B1-A11
Method BLASTX
NCBI GI g4220474
BLAST score 294
E value 1.0e-26
Match length 102
% identity 54
NCBI Description (AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No. 34887
Seq. ID LIB3030-007-Q1-B1-A12
Method BLASTX
NCBI GI g4335857
BLAST score 344
E value 2.0e-32
Match length 126
% identity 50
NCBI Description (AF049347) berberine bridge enzyme [Berberis stolonifera]

Seq. No. 34888
Seq. ID LIB3030-007-Q1-B1-C7
Method BLASTX
NCBI GI g2827637
BLAST score 211
E value 6.0e-17
Match length 111
% identity 40
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 34889
Seq. ID LIB3030-007-Q1-B1-D5
Method BLASTX
NCBI GI g2465923
BLAST score 272
E value 5.0e-24
Match length 122
% identity 26
NCBI Description (AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No. 34890
Seq. ID LIB3030-007-Q1-B1-E3
Method BLASTN
NCBI GI g18683
BLAST score 75
E value 5.0e-34
Match length 207
% identity 74
NCBI Description G.max N-20t gene

Seq. No. 34891

Seq. ID LIB3030-007-Q1-B1-G10
 Method BLASTX
 NCBI GI g3193316
 BLAST score 242
 E value 2.0e-20
 Match length 125
 % identity 49
 NCBI Description (AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No. 34892
 Seq. ID LIB3030-007-Q1-B1-H11
 Method BLASTX
 NCBI GI g1041706
 BLAST score 542
 E value 1.0e-55
 Match length 120
 % identity 79
 NCBI Description (U30480) expansin At-EXP6 [Arabidopsis thaliana]

Seq. No. 34893
 Seq. ID LIB3030-008-Q1-B1-A10
 Method BLASTX
 NCBI GI g2462744
 BLAST score 176
 E value 8.0e-13
 Match length 125
 % identity 31
 NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 34894
 Seq. ID LIB3030-008-Q1-B1-C9
 Method BLASTX
 NCBI GI g4415937
 BLAST score 140
 E value 1.0e-08
 Match length 108
 % identity 30
 NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No. 34895
 Seq. ID LIB3030-008-Q1-B1-G10
 Method BLASTX
 NCBI GI g2244851
 BLAST score 203
 E value 5.0e-16
 Match length 115
 % identity 40
 NCBI Description (Z97337) amine oxidase [Arabidopsis thaliana]

Seq. No. 34896
 Seq. ID LIB3030-009-Q1-B1-A1
 Method BLASTN
 NCBI GI g3059094
 BLAST score 166
 E value 2.0e-88
 Match length 328

Match length 435
 % identity 94
 NCBI Description Glycine max nodulin-26 mRNA, complete cds
 Seq. No. 34902
 Seq. ID LIB3030-009-Q1-B1-C12
 Method BLASTX
 NCBI GI g2627181
 BLAST score 476
 E value 6.0e-48
 Match length 117
 % identity 74
 NCBI Description (D89619) cycloartenol synthase [Pisum sativum]

Seq. No. 34903
 Seq. ID LIB3030-009-Q1-B1-D12
 Method BLASTX
 NCBI GI g3850588
 BLAST score 527
 E value 8.0e-54
 Match length 141
 % identity 49
 NCBI Description (AC005278) Contains similarity to gb_AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF_00168. ESTs gb_AA585988 and gb_T04384 come from this gene. [Arabidopsis thaliana]

Seq. No. 34904
 Seq. ID LIB3030-009-Q1-B1-D3
 Method BLASTX
 NCBI GI g4049518
 BLAST score 195
 E value 3.0e-19
 Match length 139
 % identity 40
 NCBI Description (AL031852) conserved hypothetical protein. [Schizosaccharomyces pombe]

Seq. No. 34905
 Seq. ID LIB3030-009-Q1-B1-D8
 Method BLASTX
 NCBI GI g4510339
 BLAST score 583
 E value 2.0e-60
 Match length 147
 % identity 40
 NCBI Description (AC006921) putative ABC transporter protein [Arabidopsis thaliana]

Seq. No. 34906
 Seq. ID LIB3030-009-Q1-B1-F10
 Method BLASTX
 NCBI GI g2852449
 BLAST score 470
 E value 3.0e-47
 Match length 119
 % identity 74

NCBI Description (D88207) protein kinase [Arabidopsis thaliana] >gi_2947061
(AC002521) putative protein kinase [Arabidopsis thaliana]

Seq. No. 34907
Seq. ID LIB3030-009-Q1-B1-F3
Method BLASTX
NCBI GI g280401
BLAST score 508
E value 1.0e-51
Match length 130
% identity 73
NCBI Description H⁺-transporting ATPase (EC 3.6.1.35) - curled-leaved
tobacco >gi_170206 (M27888) H⁺-translocating ATPase
[Nicotiana plumbaginifolia]

Seq. No. 34908
Seq. ID LIB3030-009-Q1-B1-H4
Method BLASTX
NCBI GI g2578440
BLAST score 142
E value 4.0e-09
Match length 73
% identity 37
NCBI Description (X67425) pectinesterase [Pisum sativum]

Seq. No. 34909
Seq. ID LIB3030-009-Q1-B1-H8
Method BLASTX
NCBI GI g4105782
BLAST score 156
E value 2.0e-10
Match length 41
% identity 80
NCBI Description (AF049922) PGP169-12 [Petunia x hybrida]

Seq. No. 34910
Seq. ID LIB3030-010-Q1-B1-A9
Method BLASTX
NCBI GI g2833329
BLAST score 443
E value 3.0e-44
Match length 99
% identity 36
NCBI Description ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE
NUCLEOTIDE TRANSLOCATOR) (ANT) >gi_1438860 (L11618) ADP/ATP
carrier protein [Anopheles gambiae] >gi_1438862 (L11617)
ADP/ATP carrier protein [Anopheles gambiae]

Seq. No. 34911
Seq. ID LIB3030-010-Q1-B1-C9
Method BLASTX
NCBI GI g131199
BLAST score 158
E value 1.0e-10
Match length 110
% identity 40
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR

% identity 83
NCBI Description Soybean hydroxyproline-rich glycoprotein (sbHRGP2) mRNA, 3' end

Seq. No. 34917
Seq. ID LIB3030-011-Q1-B1-E11
Method BLASTX
NCBI GI g4056506
BLAST score 565
E value 2.0e-58
Match length 136
% identity 74

NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 34918
Seq. ID LIB3030-011-Q1-B1-H3
Method BLASTN
NCBI GI g170455
BLAST score 52
E value 9.0e-21
Match length 148
% identity 84

NCBI Description Tomato heat shock cognate protein 80 gene, 3' end

Seq. No. 34919
Seq. ID LIB3030-012-Q1-B1-C10
Method BLASTX
NCBI GI g128592
BLAST score 149
E value 6.0e-10
Match length 54
% identity 57

NCBI Description POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR
>gi_82190_pir_S22495 pollen-specific protein precursor - common tobacco >gi_19902_emb_CAA43454_ (X61146) pollen specific protein [Nicotiana tabacum]

Seq. No. 34920
Seq. ID LIB3030-012-Q1-B1-C6
Method BLASTX
NCBI GI g2511693
BLAST score 166
E value 4.0e-12
Match length 58
% identity 55

NCBI Description (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No. 34921
Seq. ID LIB3030-012-Q1-B1-D9
Method BLASTN
NCBI GI g1055367
BLAST score 191
E value 1.0e-103
Match length 319
% identity 90

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No. 34922
 Seq. ID LIB3030-012-Q1-B1-E8
 Method BLASTX
 NCBI GI g2832646
 BLAST score 178
 E value 5.0e-13
 Match length 78
 % identity 38
 NCBI Description (AL021710) MuDR transposable element - like protein
 [Arabidopsis thaliana]

Seq. No. 34923
 Seq. ID LIB3030-012-Q1-B1-F10
 Method BLASTX
 NCBI GI g1705463
 BLAST score 372
 E value 8.0e-36
 Match length 117
 % identity 66
 NCBI Description BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi_2129547_pir_S71201
 biotin sythase - Arabidopsis thaliana >gi_1045316 (U24147)
 biotin sythase [Arabidopsis thaliana] >gi_1403662 (U31806)
 BIO2 protein [Arabidopsis thaliana] >gi_1769457 (L34413)
 biotin synthase [Arabidopsis thaliana] >gi_2288983
 (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana]
 >gi_1589016_prf_2209438A biotin synthase [Arabidopsis
 thaliana]

Seq. No. 34924
 Seq. ID LIB3030-012-Q1-B1-H10
 Method BLASTX
 NCBI GI g4006915
 BLAST score 250
 E value 2.0e-21
 Match length 109
 % identity 50
 NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No. 34925
 Seq. ID LIB3030-012-Q1-B1-H3
 Method BLASTX
 NCBI GI g3600039
 BLAST score 487
 E value 4.0e-49
 Match length 143
 % identity 61
 NCBI Description (AF080119) similar to Schizosaccharomyces pombe isp4
 protein (GB:D14061) [Arabidopsis thaliana]

Seq. No. 34926
 Seq. ID LIB3039-001-Q1-E1-E2
 Method BLASTN
 NCBI GI g168650
 BLAST score 226
 E value 1.0e-124
 Match length 351

% identity 93
NCBI Description Zea mays ubiquitin fusion protein (UBF9) gene, complete cds

Seq. No. 34927
Seq. ID LIB3039-001-Q1-E1-F7
Method BLASTX
NCBI GI g1405561
BLAST score 276
E value 2.0e-24
Match length 56
% identity 98
NCBI Description (X98540) FSGTP1 [Fagus sylvatica]

Seq. No. 34928
Seq. ID LIB3039-001-Q1-E1-F8
Method BLASTX
NCBI GI g3341443
BLAST score 293
E value 1.0e-29
Match length 116
% identity 61
NCBI Description (AJ223074) acid phosphatase [Glycine max]

Seq. No. 34929
Seq. ID LIB3039-001-Q1-E1-H8
Method BLASTN
NCBI GI g170091
BLAST score 64
E value 9.0e-28
Match length 180
% identity 84
NCBI Description Glycine max vegetative storage protein (vspB) gene, complete cds

Seq. No. 34930
Seq. ID LIB3039-002-Q1-E1-A10
Method BLASTX
NCBI GI g3341443
BLAST score 315
E value 4.0e-29
Match length 114
% identity 56
NCBI Description (AJ223074) acid phosphatase [Glycine max]

Seq. No. 34931
Seq. ID LIB3039-002-Q1-E1-A11
Method BLASTN
NCBI GI g169974
BLAST score 122
E value 4.0e-62
Match length 350
% identity 84
NCBI Description Glycine max vspA gene, complete cds

Seq. No. 34932
Seq. ID LIB3039-002-Q1-E1-A9
Method BLASTN

% identity 55
 NCBI Description (AJ223074) acid phosphatase [Glycine max]

Seq. No. 34949
 Seq. ID LIB3039-004-Q1-E1-B5
 Method BLASTX
 NCBI GI g2052379
 BLAST score 142
 E value 5.0e-09
 Match length 69
 % identity 45
 NCBI Description (U66343) calreticulin [Arabidopsis thaliana]

Seq. No. 34950
 Seq. ID LIB3039-004-Q1-E1-C3
 Method BLASTX
 NCBI GI g232031
 BLAST score 191
 E value 1.0e-14
 Match length 97
 % identity 46
 NCBI Description ELONGATION FACTOR 1 BETA' >gi_322851_pir_S29224
 translation elongation factor eEF-1 beta' chain - rice
 >gi_218161_dbj_BAA02253_(D12821) elongation factor 1 beta'
 [Oryza sativa]

Seq. No. 34951
 Seq. ID LIB3039-004-Q1-E1-E3
 Method BLASTX
 NCBI GI g3687251
 BLAST score 420
 E value 3.0e-41
 Match length 118
 % identity 69
 NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]

Seq. No. 34952
 Seq. ID LIB3039-005-Q1-E1-A6
 Method BLASTX
 NCBI GI g3341443
 BLAST score 305
 E value 7.0e-28
 Match length 121
 % identity 51
 NCBI Description (AJ223074) acid phosphatase [Glycine max]

Seq. No. 34953
 Seq. ID LIB3039-005-Q1-E1-A9
 Method BLASTN
 NCBI GI g169974
 BLAST score 173
 E value 1.0e-92
 Match length 253
 % identity 92
 NCBI Description Glycine max vspA gene, complete cds

Seq. No. 34954

NCBI Description (AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No. 34987
Seq. ID LIB3039-009-Q1-E1-D9
Method BLASTN
NCBI GI g18551
BLAST score 322
E value 0.0e+00
Match length 382
% identity 96
NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding protein

Seq. No. 34988
Seq. ID LIB3039-009-Q1-E1-E11
Method BLASTN
NCBI GI g169974
BLAST score 262
E value 1.0e-145
Match length 382
% identity 92
NCBI Description Glycine max vspA gene, complete cds

Seq. No. 34989
Seq. ID LIB3039-009-Q1-E1-F12
Method BLASTX
NCBI GI g134145
BLAST score 156
E value 2.0e-10
Match length 101
% identity 25
NCBI Description STEM 28 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE PROTEIN A) >gi_99886_pir_S08511 28K protein - soybean >gi_169898 (M37530) 28 kDa protein [Glycine max] >gi_169975 (M76981) vegetative storage protein [Glycine max] >gi_226867_prf_1609232B 28kD glycoprotein [Glycine max] >gi_444325_prf_1906374A vegetative storage protein [Glycine max]

Seq. No. 34990
Seq. ID LIB3039-009-Q1-E1-F6
Method BLASTX
NCBI GI g3341443
BLAST score 261
E value 7.0e-23
Match length 81
% identity 59
NCBI Description (AJ223074) acid phosphatase [Glycine max]

Seq. No. 34991
Seq. ID LIB3039-009-Q1-E1-G4
Method BLASTN
NCBI GI g435678
BLAST score 37
E value 1.0e-11
Match length 53

% identity 92
NCBI Description L.esculentum Mill (cv. Rutgers) mRNA for ribosomal protein
S25

Seq. No. 34992
Seq. ID LIB3039-009-Q1-E1-H3
Method BLASTX
NCBI GI g548774
BLAST score 166
E value 9.0e-12
Match length 60
% identity 62
NCBI Description 60S RIBOSOMAL PROTEIN L7A >gi_542158_pir_S38360 ribosomal
protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
ribosomal protein L7A [Oryza sativa]

Seq. No. 34993
Seq. ID LIB3039-010-Q1-E1-A10
Method BLASTN
NCBI GI g1262439
BLAST score 341
E value 0.0e+00
Match length 357
% identity 99
NCBI Description Glycine max lipoxxygenase (vlxC) mRNA, complete cds

Seq. No. 34994
Seq. ID LIB3039-010-Q1-E1-A12
Method BLASTX
NCBI GI g421867
BLAST score 277
E value 8.0e-25
Match length 89
% identity 67
NCBI Description ubiquitin / ribosomal protein CEP52 - turnip >gi_347064
(L21898) ubiquitin/ribosomal protein [Brassica rapa]
>gi_395079_emb_CAA80863_ (Z24738) ubiquitin/ribosomal
protein [Brassica rapa]

Seq. No. 34995
Seq. ID LIB3039-010-Q1-E1-B9
Method BLASTX
NCBI GI g120666
BLAST score 200
E value 4.0e-25
Match length 99
% identity 60
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
>gi_66012_pir_DESKG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - garden snapdragon

Seq. No. 34996
Seq. ID LIB3039-010-Q1-E1-C10
Method BLASTN
NCBI GI g170091
BLAST score 202
E value 1.0e-110

BLAST score 315
 E value 1.0e-177
 Match length 379
 % identity 96
 NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35002
 Seq. ID LIB3039-010-Q1-E1-F7
 Method BLASTX
 NCBI GI g3341443
 BLAST score 143
 E value 3.0e-09
 Match length 69
 % identity 45
 NCBI Description (AJ223074) acid phosphatase [Glycine max]

Seq. No. 35003
 Seq. ID LIB3039-010-Q1-E1-G1
 Method BLASTX
 NCBI GI g541943
 BLAST score 179
 E value 3.0e-15
 Match length 56
 % identity 79
 NCBI Description metallothionein - soybean >gi_228682_prf_1808316A
 metallothionein-like protein [Glycine max]

Seq. No. 35004
 Seq. ID LIB3039-010-Q1-E1-G7
 Method BLASTX
 NCBI GI g2431771
 BLAST score 156
 E value 1.0e-10
 Match length 51
 % identity 61
 NCBI Description (U62753) acidic ribosomal protein P2b [Zea mays]

Seq. No. 35005
 Seq. ID LIB3039-010-Q1-E1-H1
 Method BLASTN
 NCBI GI g169974
 BLAST score 235
 E value 1.0e-129
 Match length 303
 % identity 94
 NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35006
 Seq. ID LIB3039-010-Q1-E1-H5
 Method BLASTN
 NCBI GI g169974
 BLAST score 145
 E value 8.0e-76
 Match length 277
 % identity 91
 NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35012
 Seq. ID LIB3039-011-Q1-E1-E6
 Method BLASTX
 NCBI GI g2961372
 BLAST score 140
 E value 9.0e-09
 Match length 97
 % identity 34
 NCBI Description (AL022141) putative ribosomal protein L8 [Arabidopsis thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No. 35013
 Seq. ID LIB3039-011-Q1-E1-E9
 Method BLASTN
 NCBI GI g170091
 BLAST score 289
 E value 1.0e-162
 Match length 369
 % identity 95
 NCBI Description Glycine max vegetative storage protein (vspB) gene, complete cds

Seq. No. 35014
 Seq. ID LIB3039-011-Q1-E1-F7
 Method BLASTN
 NCBI GI g170091
 BLAST score 245
 E value 1.0e-135
 Match length 357
 % identity 92
 NCBI Description Glycine max vegetative storage protein (vspB) gene, complete cds

Seq. No. 35015
 Seq. ID LIB3039-012-Q1-E1-A11
 Method BLASTN
 NCBI GI g169974
 BLAST score 54
 E value 6.0e-22
 Match length 158
 % identity 84
 NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35016
 Seq. ID LIB3039-012-Q1-E1-C3
 Method BLASTX
 NCBI GI g1076510
 BLAST score 186
 E value 3.0e-14
 Match length 58
 % identity 64
 NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean >gi_829119_emb_CAA52414_ (X74403) cyclophilin [Phaseolus vulgaris]

Seq. No. 35017
 Seq. ID LIB3039-012-Q1-E1-C8
 Method BLASTN
 NCBI GI g169974
 BLAST score 159
 E value 2.0e-84
 Match length 259
 % identity 90
 NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35018
 Seq. ID LIB3039-012-Q1-E1-D4
 Method BLASTX
 NCBI GI g3341443
 BLAST score 224
 E value 3.0e-20
 Match length 94
 % identity 59
 NCBI Description (AJ223074) acid phosphatase [Glycine max]

Seq. No. 35019
 Seq. ID LIB3039-012-Q1-E1-D5
 Method BLASTX
 NCBI GI g4006867
 BLAST score 178
 E value 3.0e-13
 Match length 67
 % identity 55
 NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 35020
 Seq. ID LIB3039-012-Q1-E1-E1
 Method BLASTX
 NCBI GI g2961300
 BLAST score 210
 E value 6.0e-17
 Match length 84
 % identity 52
 NCBI Description (AJ225027) ribosomal protein L24 [Cicer arietinum]

Seq. No. 35021
 Seq. ID LIB3039-012-Q1-E1-E12
 Method BLASTX
 NCBI GI g3341443
 BLAST score 216
 E value 2.0e-17
 Match length 88
 % identity 49
 NCBI Description (AJ223074) acid phosphatase [Glycine max]

Seq. No. 35022
 Seq. ID LIB3039-012-Q1-E1-E2
 Method BLASTN
 NCBI GI g456713
 BLAST score 105
 E value 4.0e-52
 Match length 291

% identity	46
NCBI Description	Glycine max gene for ubiquitin, complete cds

```
Seq. No.      35023
Seq. ID       LIB3039-012-Q1-E1-E9
Method        BLASTN
NCBI GI       g170091
BLAST score    193
E value       1.0e-104
Match length   356
% identity     97
NCBI Description Glycine max vegetative storage protein (vspB) gene,
                  complete cds
```

```
Seq. No.      35024
Seq. ID      LIB3039-012-Q1-E1-F11
Method       BLASTN
NCBI GI      g410285
BLAST score   100
E value      6.0e-49
Match length  211
% identity    87
NCBI Description Pisum sativum rho (ras-related) GTP-binding protein mRNA,
                complete cds
```

```
Seq. No.      35025
Seq. ID      LIB3039-012-Q1-E1-F7
Method       BLASTN
NCBI GI      g1336081
BLAST score   73
E value      7.0e-33
Match length  325
% identity   82
NCBI Description Glycine max var. Century ascorbate peroxidase 2 (APx2)
                mRNA, complete cds
```

```
Seq. No.          35026
Seq. ID           LIB3039-012-Q1-E1-H2
Method            BLASTN
NCBI GI           g169974
BLAST score       231
E value           1.0e-127
Match length      355
% identity        91
NCBI Description   Glycine max vspA gene, complete cds
```

```
Seq. No.      35027
Seq. ID      LIB3039-013-Q1-E1-A4
Method       BLASTX
NCBI GI      g4538965
BLAST score   180
E value      3.0e-13
Match length  87
% identity    45
NCBI Description (AL049488) hypothetical protein [Arabidopsis thaliana]
```

Seq. No. 35028

E value 4.0e-83
 Match length 208
 % identity 94
 NCBI Description Glycine max vspA gene, complete cds

Seq. No. 35034
 Seq. ID LIB3039-014-Q1-E1-F8
 Method BLASTX
 NCBI GI g4127352
 BLAST score 321
 E value 9.0e-30
 Match length 122
 % identity 48
 NCBI Description (AJ010451) glutathione transferase [Alopecurus myosuroides]

Seq. No. 35035
 Seq. ID LIB3039-014-Q1-E1-H12
 Method BLASTX
 NCBI GI g3292849
 BLAST score 317
 E value 3.0e-29
 Match length 85
 % identity 72
 NCBI Description (AJ007582) arginine methyltransferase [Arabidopsis thaliana]

Seq. No. 35036
 Seq. ID LIB3039-015-Q1-E1-A4
 Method BLASTX
 NCBI GI g2558962
 BLAST score 169
 E value 4.0e-12
 Match length 75
 % identity 49
 NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]

Seq. No. 35037
 Seq. ID LIB3039-015-Q1-E1-B9
 Method BLASTX
 NCBI GI g488573
 BLAST score 242
 E value 1.0e-20
 Match length 81
 % identity 63
 NCBI Description (U09463) histone H3.2 [Medicago sativa]

Seq. No. 35038
 Seq. ID LIB3039-015-Q1-E1-C5
 Method BLASTX
 NCBI GI g134145
 BLAST score 144
 E value 2.0e-09
 Match length 44
 % identity 64
 NCBI Description STEM 28 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE PROTEIN A) >gi_99886_pir_S08511 28K protein - soybean >gi_169898 (M37530) 28 kDa protein [Glycine max] >gi_169975

BLAST score 180
 E value 2.0e-13.
 Match length 69
 % identity 54
 NCBI Description (AC003970) Highly similar to cinnamyl alcohol
 dehydrogenase, gi_1143445 [Arabidopsis thaliana]

Seq. No. 35050
 Seq. ID LIB3039-017-Q1-E1-H10
 Method BLASTN
 NCBI GI g170091
 BLAST score 329
 E value 0.0e+00
 Match length 361
 % identity 98
 NCBI Description Glycine max vegetative storage protein (vspB) gene,
 complete cds

Seq. No. 35051
 Seq. ID LIB3039-017-Q1-E1-H9
 Method BLASTX
 NCBI GI g3341443
 BLAST score 235
 E value 1.0e-19
 Match length 98
 % identity 52
 NCBI Description (AJ223074) acid phosphatase [Glycine max]

Seq. No. 35052
 Seq. ID LIB3039-018-Q1-E1-A4
 Method BLASTN
 NCBI GI g558922
 BLAST score 67
 E value 3.0e-29
 Match length 179
 % identity 92
 NCBI Description Lupinus albus farnesyl pyrophosphate synthase (fps1) mRNA,
 complete cds

Seq. No. 35053
 Seq. ID LIB3039-018-Q1-E1-B10
 Method BLASTX
 NCBI GI g3341443
 BLAST score 324
 E value 4.0e-30
 Match length 113
 % identity 58
 NCBI Description (AJ223074) acid phosphatase [Glycine max]

Seq. No. 35054
 Seq. ID LIB3039-018-Q1-E1-C9
 Method BLASTX
 NCBI GI g4262140
 BLAST score 170
 E value 4.0e-12
 Match length 68
 % identity 54